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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1905)
Elliott,R.C., Betzner,A.S., Huttner,E., Oakes,M.P., Tucker,W.Q.,
Gerentes,D., Perez,P. and Smyth,D.R.
ANWIEGUMENTA, an APETALA2-like gene of Arabidopsis with pleiotropic roles in ovule development and floral organ growth
Plant Cell 8 (2), 155-168 (1996)
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Monash University, Wellington Road, Clayton,
Location/Qualifiers
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Arabidopsis thaliana ANT (AINTEGUMENTA) mRNA,
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                                                                                                                                  /note="similar to APETALA2 protein encoded by GenBank Accession Number U12546"
                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="Landsberg erecta"
/db xref="taxon:3702"
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/db_xref="GI:1244708"
/transiation="MKSFCDNDDNNHSNTTNLLGFSLSSNWMKWGGRGGREAIYSSST
                                                                                        product = "ANT
                                                                                                                                                                                                                                           gene="AINTEGUMENTA"
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/tissue_type="flower; ovule"
1. .1905
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Clayton, VIC 3168, Australia
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                        198 GlyLeuLysAsnTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGlu 217
                                                                             542 GARACT----AGARATTACGGGAATGAC-
                                                                                                                            178 GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu 197
                                                                                                                                                                                                                                   158 ThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuGluGlu 177
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REFERENCE AUTHORS TITLE

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PEATURES

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------GAGGAA 541

-GAGCCCAACACG

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CCTAGTTTGACACAT 580

JOURNAL

REFERENCE AUTHORS

TITLE

SOURCE ORGANISM

KEYWORDS

RESULT 8 ATU41339 LOCUS

DEFINITION VERSION CCESSION

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ORIGIN Best Local Similarity: Score: US-10-024-632-2 (1-663) x ATU41339 (1-1905) Query Match: Percent Similarity: Alignment Scores: misc_feature misc_feature 30 -----38 ATGAAGTCTTTTTGTGATAATGATGATAATAATCATAGCAACACGACTAATTTGTTAGGG 21 PheSerLeuSerProHis---MetLysMet----------------1 MetLysArgIleAsnGluSerAsnAsnThrAspAspGlyAsnAsnHisAsnTrpLeuGly TTCTCATTGTCTTCAAATATGATGAAAATGGGGAGGTAGAGGAGGTAGAGAAGCTATTTAC 157 1184. .1391 SSHSNHHQDSSPKVEDFFGTHHNNTSHKEAMDLSLDSLFYNTTHEPNTTTNFQEFFSF PQTRNHEEETRNYGNDPSLTHGGSFNVGVYGEFQQSLSLSMSPGSQSSCITGSHHHQQ NQNQNHQSQNHQQISEALVETSVGFETTTNAAAKKKRGQEDVVVVGQKQIVHRKSIDT RIMSSNTLLSGELARNNNSIVVRNTEDQTALNAVVEGGSNKEVSTPERLLSFPAIFA LPQVNQKMFGSNMGGNMSPWTSNPNAELKTVALTLPQMPVFAAWADS" fgortsoyrgvtrhrwtgryeahlmdnsfkkeghsrkgrovylggydmekkaaraydl aalkywgpsthtnfsaenyokeiedmknmtroeyvahlrrkssgfsrgasiyrgvtrh hohgrwoarigrvagnkdlylgtfgtoeeaaeaydvaaikfrgtnavtnfditrydvd SSAATSSSSVPPQLVVGDNTSNFGVCYGSNPNGGIYSHMSVMPLRSDGSLCLMEALNR gene="AINTEGUMENTA" /gene="AINTEGUMENTA" /note="encodes first AP2 domain" note="ecodes second 6.66e-81 1328.00 52.84% 43.27% 37.92% ---GluAlaThrSerAlaAlaThrValProThrThrPheTyrMet 43 Length: Matches: Gaps: Indels: Mismatches: Conservative: AP2 domain" 97

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spProArgAsnLysAs	68 CTCTACCTTGGA	1088 GAGAATTATCAGAAAGA 386 HisLeuargargLysse	326 Thx 968 AGT 346 Ala 346 GCP 366 Glv	06 88 80	8
pileAspTyrAsnLysSerValValThrSerValAsnAsnGl	TGGAACCCAAGAAGAAGCTGCAGAAGCTTACGATGTAGCAGCA 13 AABDALAVAITHASHDheAsplleSerArgTyrAspValGlu 46 AAATGCTGTAGCACAACTTTGATATCACGAGGTACGATGTTGAT 13 AAATGCTGTGACACTACCTTGATATCACGAGGTACGATGTTGAT 13 FABILEULEUAlaGlyGluLeuAlaArgArgTysLysAspAsn 48 FABILEULEUALGGLYGLULEUALAARGTAGGAAC	AGACAAGAATATGTTGC IleTyrargGlyValTh ATCTATAGAGGAGTCAC ATCTATAGAGGAGTCAC ATCTATAGAAGAAGTAAAAAAAAAA	4000	ASPALDY SLYBALGELY MISSES	yAsnGluargasnGlyValSerLeuGlySerValGly 23 .TGGGGAATTTCAA

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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N;Alternate names: AP2 domain-containing protein; protein T28I19.30
C;Epecies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 22-Oct-1999
C;Accession: S71365; T06022
R;Klucher, K.
submitted to the EMBL Data Library, November 1995
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A;Accession: T06022
A;Molecule type: DNA
A;Residues: 1-555 <BEV>
A;Cross-references: EMBL:AL035709; GSPDB:GN00062; ATSP:T28I19.30
A;Experimental source: cultivar Columbia; BAC clone T28I19
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A; Introns: 111/1; 289/2; 317/1; 320/1; 349/3; 391/2; 417/1
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                                                                                                                                                                                                                                                                                                                                                                    MKSFCDNDDNNHSNTTNLLGFSLSSNMMKMGGRGGREAIYSSSTSSAATSSSSVPPQLVV
                                                                                                                                                             THPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE 217
                                                                                                                                                                                                           DFFG----THHNNTSHKEAMDLSLDSLFYNTTH---EPNTTTNFOEFFSFPQTRNH----
                                              -----GSFNVGV-----YGEFQQSLSLSMSPGSQSSCITGSHHHQQNQNQNHQSQNH 229
                                                                                    QQMNCGMGNERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTAPS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       113; Indels 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 555;
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C;Accession: B96750

R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, G. A; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: B96750

A;Residues: 1-425 <STO>
A;Accession: B968405173; NID:96648171; PIDN:AAF21171.1; GSPDB:GN00141
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B96750
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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Best Local
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Local Similarity 43.4%;
nes 214; Conservative 6
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                                      132 SQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKETHVSDCSSL
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                                                                                                                                                                                                 WLGFSLSPHMKM-----EATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDPRNKDIDYNKSVVISVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSDQ 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLYLGTFGTQEEAAEAYDVAAIKFRGTNAVTNFDITRYDVDRIMSSNTLLSGELARRN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLYLGTFSTQEEAAEAYDVAAIKFRGANAVINFDISRYDVERIMASSNLLAGELARRKKD 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AENYOKE I EDMKNMTROEYVAHLRRKSSGFSRGAS I YRGVTRHHOHGRWQAR I GRVAGNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRWTGRYEAHLWDNSFKKEGHSRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFS
                                                                                                                                                             WLGFSLTPPLRICNSEEEELRHDGSDGTLFF-----
QTNVNCTTVVNRLNPP--
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                                                                                                                                                                                                                                     ; Score 923.5; DB 2; pred. No. 1.5e-57; 60; Mismatches 108;
                                                                                                                                                                                                                                            Indels
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    -LHDQTVVTPHY---
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      109
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A;Cross-references: EMBL:AL391142
A;Experimental source: cultivar Columbia; BAC clone T10B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, submitted to the Protein Sequence Database, August 2000 A;Reference number: Z25394
A;Accession: T51580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovule development protein aintegumenta-like protein - Arabidopsis thaliana N;Alternate names: protein T1086 90 C;Species: Arabidopsis thaliana Tmouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000 C;Accession: T51580
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A;Map position: 5
A;Introns: 78/1; 216/2; 244/1; 273/3; 298/2; 315/2; 341/1
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A; Molecule type: DNA
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Best Local S
Matches 255
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                       290 DTFGQRTSQYRGYTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPQMTEG----
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                                                                                                                                                                                                                                                                                                                                              SDGSLCI-LEALKRSQTQVMVPTSSP---KLEDFLGGATMGTHEYGSHER-----GLSLD 126
                                                                                                                                                                                                                                                                                                                                                                                      NNWLGFSLSPH----
                                                           SVANANHQDNGNGARGLSL&MNSSTSDSNNYNNNDDV---VQEKTIVDVVZTTP--KKTI
                                                                                                                                                                              DCSSIMPQMTEGIKNWVAPTRE-FSTHQQVLEQQMNCGMGNERNGVSLG------
                                                                                                                                                                                                                                                               SIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKETHVS 186
                                                                                                                                                                                                                                                                                                          VAGGYCFDLAAPSDESSAVQTSFLSPFGVTLEAF-----TRDNNSHSRDWDINGGACN
                                                                                                                                              -----PK----LENFLGRTTTIYNTNETVVDGNGDCGGGDGGGGGSLGLSMIKTWLSNH 146
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.2%; Score 916.5; DB 2; 35.2%; Pred. No. 7.5e-57; tive 76; Mismatches 170;
                                                                                                      --SLSLSMSPGSQSSCVTAPSGTDSVAVDAKKRGHAKLGQKQPVHRKSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282
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                                                                                                                                                                                       234
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QY 264 DSVAVDAKKRGHAKLGOKOPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKE 323	Strain Black Mexican Swe 25.4%; Score 890; D 44.2%; Pred. No. 4.2 vative 45; Mismatches TEGIKNWVAPTREFSTHQQVLEQQHLSFSISNNVYHHGLLEAFCGELGSLSL SRRLQIRITSLCAASCGSITARFL		379 SPSLPIGSSAKRLKD	Db 202 ESFGQRTSIYRGVTRHRWTGRYEAHLWDNSCKREGQTRKGRQGGYDKEEKAARAYDL 258 OY 350 AALKYWGPSTHINFSIENYQVQLEEWKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQ 409
The distribution of the blank o	ELWDNSCRE	A; MSCALL C. F. C.	PSSULT 5 P96549 hypothetical protein F11M15.6 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text_change 31-Mar-2001 C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text_change 31-Mar-2001 C;Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Hulzar, L.; A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference number: As6141; MUID:21016719; PMID:11130712 A;Status: preliminary A.M.; Sun, H.; Tallon A;Status: preliminary	Db 286 AAIKFRGLNAVTNLDMSRYDVESILSSDLPVGGGASGRAAAKFPLDSLQPGSAAAMMIAG 345 Qy 477 ELARRKKDNDPRNKDI

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RESULT 6
T49988
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A;Residues: 1-566 <BEV>
A;Cross-references: EMBL:AL353995; GSPDB:GN00063; ATSP:F12B17.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z25026
A; Accession: T49988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T49988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ovule development protein-like - Arabidopsis thaliana
N;Alternate names: protein F12B17.140
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 33/1; 259/2; 287/1; 316/3; 341/2; 384/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: cultivar Columbia; BAC clone F12B17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bevan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: ATSP:F12B17.140
                                                                                                                                                                                                                                                                                                                                                                          405
                                                                                     521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 RKSI-DTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKSGQTRKGRQVYLGGYDMEEKAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 SPLTVMPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDFLGGATMGTHEYGSHERGLSLD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 NNHNWLGFSLSPHMKMEATSAA-----TVPTTFYMSPSQSHLSNFGMCYGVGENGNFH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                     SEWKM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKKIADTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQARKGRQ---GGYDKEDKAA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GALSLGVNVNNNTNHRNDNDNHYRGNNNGERINNNNNNDNEKTDSEKEKAVVAVETSDCS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGEL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-SSTVGSSAEEEFPAVKVDYDMPP 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLSSSREASPEKRGPSLL--FPMPP 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NN-----YLQSSSHTSQLYNAYLQSNPGL-----LHGFVSDNNNTSGFLGNNGIGIG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVT 596
                                                                                                                                                                                                                                                                                                                                               TRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDV 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFYGWSNQKPQEFFKEEAQLAAAASMADSTILTTF-VDP-QSH----------
       INFALCENSAVQSQQIIPCGIPFEAAALYHHHQQQQQHQQQQQQQNFFQ--HFPANAAS- 533
                                                                                                                                                                                                                                                                                                                                                                                                                                         RAYDLAALKYWNATATTNFPITNYSKEVEENKHWIKQEFIASLRRKSSGFSRGASIYRGV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSLSLSMSPGSQSS------CVTAPSGTDSVAVDAKKRGHAKLGQKQPVH 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSEVDDSASIGRTHLAG-----DYLGHVV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAIMKSALPIGGAAKRIKLSLEAAASSEQKPILGHHQLHHFQQQQQQQQQQQQQQQQX
                                                                                                                                                                                                                              ERIMASSNLLAGELARRKKOND----PRNKDIDYNKSVVTSVNNEETVQVQAGNNNNEND 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGV 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIVRYSDNSQTDTQDSSLTQIYDFRHHHN-QTGFYSDHHDFKTMA--GFQSA---FSTNS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQT----HPYYSGLACHGLYQAPLEEETTK 181
                                                                                                                                                                                                                                                                                                    TRHHQQGRWQARIGRVAGNKDLYLGTFATEEEAAEAYDIAAIKFRGINAYTNFEMNRYDV 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69; Mismatches 167; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 831; DB 2
Pred. No. 8e-51;
                                                                              ---VLFNHPSQQQQANGNGSDQKIMNCGNYRNSAFSM 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lemcke, K.; Mayer, K.F.X
2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ESSGPELGFHG-GST 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T24D18.16 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Bate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: D86295
C;Acce
В
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A; Residues: 1-332 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                                                                                                          H96827
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB:AE005172; NID:g6587812; PIDN:AAF18503.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 18.4%; Score 645; DB 2 Local Similarity 46.4%; Pred. No. 5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 DQKI 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 SDLSPFIKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 KDNDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 YOVQLEEMKNMSROEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLY 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 PPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 TGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 SQSSCYTAPSGTD----SVAVDAKKRGHAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRW 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          534 -----DSTGSNNNS 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560 ALQDLIGIDSVGSGQHN 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGTYATQEEAAIAYDIAAIEYRGLNAVTNFDISRYLKLEVPENPIDTANNLLESP----H 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEEDIKEMESQSKEEYIGSLRRKSSGFSRGVSKYRGVAKHHHNGRWEARIGRVFGNKYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKKTSVENETGDDQSATSVVLKAKRKRRSQPRDAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRY-----DVERIMASSNLLAGELARRK 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGRYEAHLWDKNSWNETQTKKGRQ---GAYDEEDAAARAYDLAALKYWGRDTILNFPLCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NHESDLSQSQSSSEDNDDRKTKLLKSSPLVAEEVIGPST 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORSSVHRGVTRHRW
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RESULT 9
594116
594116
hypothetical protein - maize
c,Species: Zea mays (maize)
c,Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997
c,Accession: S54116
R,Daniell, T.J.; Edwards, R.
submitted to the EMBL Data Library, January 1995
A,Description: Complementation of a heat shock sensitive mutant of Escheric A,Reference number: S54116
A,Accession: S54116
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A;Accession: H96927
A;Status: preliminary A;Status: preliminary A;Molecule type: DNA A;Residues: 1-308 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-485 <DAN>
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                                               329
                                                                                                                                                                                                                                                        235 SVGC-GELQSLSLSMSPGSQSSCVTAPSGTDSVAVDAKKRGHAKLGQK-----QPVHR-- 286
                                                                                                                                                                                                                                                                                                                                                            187 DCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCG---MGNERNGVS-----LG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 HIWDNSCKKEGOTRKGROVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYOVOLE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 SSCVTAPSGTDSVAVDAKKRGHAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132;
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                                                                                                                                                                                                        58 GVGCVGAPRSRRLQIR-----ITSLCAASCGSITARFLRHYPAAQSGTTVGEPLSRFT 110
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GROVYLGGYDKEEKAARAYDLAALKFWGPTTTTNFQVSNYEKELEEMKSMTRQEFIASLR
                                               GROVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLR 388
                                                                                                    LAAMSSTDVAWAESDQASGPPRRSASAHPSTVASPGTGGRGDMRRTCGNNSCRREGQSRK 170
                                                                                                                                                   ----KSIDTFGQRTSQYRGVTR-----HRWT-----GRYEAHLWDNSCKKEGQTRK 328
                                                                                                                                                                                                                                                                                                             DMSSAYPH------HWLSFSLSNNYHHGLLEAFSNSSGTPLGDEQGAVEESPRTVEDFLG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SREPESSODNK----SPKSEEVIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEEAAIAYDIAAIEYRGLNAVTNFDVSRY-----LNPNAAADKADSDSKPIRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEEAAEAYDVAAIKFRGANAYTNFDISRYDVERIMASSNLLAGELARRKKONDPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMEGQSKEEYIGSLRRKSSGFSRGVSKYRGVARHHHNGRWEARIGRVFGNKYLYLGTYAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFST 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLWDKNSWNDTQTKKGRQ---GAYDEEEAAARAYDLAALKYWGRDTLLNFPLPSYDEDVK
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     15.2%; Score 534; DB 2; Length 485; 33.5%; Pred. No. 6.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                              48; Mismatches 146; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
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aintegumaenta-like protein - Arabidopsis thaliana
N,Alternate names: protein T12E18.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47591
R;Bloecker, H; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat N submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24469
A;Accession: T47591
A;Scratus: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <BLO-
A;Cross-references: EMBL;AL132971
A;Experimental source: cultivar Columbia; BAC clone T12E18
RESULT 11
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A; Introns: 71/2; 99/1; 128/3; 170/2
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                                                                                                                                                              120 GPDTILNFPAETYTKELEEMQRVTKEEYLASLRRQSSGFSRGVSKYRGVARHHHNGRWEA 179
                                                                                                                                                                                                                                                                                      296 TSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 GVMWGATSGAVVGQQDSSSKQGNGYASN 438
                                                                                                                                                                                                                                                                                                                                                                        241 LOSISISMSPGSQ-SSCVTAPSGTDSVAVDAKKRGHAK----LGQKQPVHRKSIDTFGQR
                                                                                                                                                                                                                                                                                                                                                                                                                109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                     RIGRVAGNKDLYLGTFST 433
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                                                                                                                                                                                                      GPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQA
                                                                                                                                                                                                                                                SSIYRGVTRHRWTGRFEAHLWDKSSWNSIQNKKGKQ---GAYDSEEAAAHTYDLAALKYW
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                                                                                                                                                                                                                                                                                                                              LTTSTCSSSPSSSVSSSTTTSSPIQSBAPRPKRAKKSSPSGDKS--HNPTSPASTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QATMPPSEKDYWSLLALHYQQQQEQERQFPASAYEAYGSGGVNVDFTMGTSSGSNNNTGS
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ilarity 55.1%;
Conservative 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 517; DB 2;
Pred. No. 2.7e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 205;
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A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Aeference number: A85001; MUID:20083488; PMID:10617198
A;Accession: A8536
A;Status: nrslim:...

Status: preliminary

APETALA2 protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (pate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: A8536 C;Accession: A8536 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999

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C;Genetics:
A;Gene: At2g41710
A;Map position: 2
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A;Cross-references: GB:
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                       probable AP2 domain transcription factor [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84845
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A;Map position: 4
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A; Residues: 1-436 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                                   A;Reference number: A84420;
A;Accession: B84845
                                                                                                                                                                                                                                                                           A_iTitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A_iReference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 YQAPLEEETTKETH------VSDCSSLMPQMTEGLK----NWVAPTREFSTHQQVLE 217
  245 SLSMSPGSQSSCVTAPSGTDSVAVDAKK-----RGHAKLGQ------KQPVHRKSIDTFG 293
                                      137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 QQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGS-----QSSCVTAPSGTDSVAVD 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 MDSNGG-----GVASG------FPRAHWFGVKFCQSDLATGSSAGKATNVA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSLGNSANS - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGMLNHTPNSNHQFPGSSNIGSGGGFSLFPAAENHRFDGRASTNQVLTNAAASSGFSPHH 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----HNQIFNSTSTPHQNWLQTNGFQPPLMRPS 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGPSLLFPMPPMETKIVNPIGTSVTSWLPSPTVQ---MRPS 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGSGQH-----NMLDESSKIGT--HFS------NTSSLVTSLSSSREASPEK 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQAGNINNENDSEWKWVLFNHESQQQQANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDS 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSTGFPRGSSKYRGVTL-HKCGRWEARMGQFLGKKYVYLGLFDTEVEAARAYDKAAIKCN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQVYLGGFDTAHAAARÄYDRAAIKFRGVEADINFNIDDYDDDLKQMTNLTKEEFVHVLRR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRR 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A----AVVEPAQPL-KKSRRGPRSRSSQYRGVTFYRRTGRWESHIWD--C-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKKRGHAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HQTQREEESEEFCYSSPSKRVGSFSNSSSSAVVIEDGSDDDELNRVRPNNPLVTHQFFPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKDAVINFDPSIYDEELNAESSG------NPTTPQDHNLD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GANAVTNFDISRYDVERIMASSNLLAGELARRKKDNDPRNKDIDYNKSVVTSVNNEETVQ 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSSGFSRGASIYRGVTRHHOHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFR 449
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:NC_001268; NID:g7270641; PIDN:CAB80358.1; GSPDB:GN00140
                                                                                                                                                                             GB:AE002093; NID:g2887500; PIDN:AAC02777.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.8%;
                                                         14.2%; Score 497.5; DB 2; 29.7%; Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %; Score 517; DB 2; Length 432;
%; Pred. No. 8.3e-29; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---KHKSQDMRLRMNQQQQD------SLHSNEVLGLGQ 343
                                    73;
                                        Mismatches
                                      168; Indels
                                                                          Length 436;
                                      83;
                                                                                                                                                                             GSPDB:GN00139
                                      Gaps
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A;Molecule type: DNA
A;Residues: 1-464 <STO>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene: At2g28550
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393 TPFLPSGSSLTSEVRSHISIEPETSEVTKTETSCSTYSYLP 433
                                                                                                                                                                                          355 GAAALSIQK--------SMYPLTSILTAPILTNYNTIDPILADPILW 392
                                                                                                                                                                                                                                                                                       555 SAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLL 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 NKSVVTSVNNEETVQVQAGNNNNENDSEWKWVLFNHPSQQQQANGNGSDQKIMNCGNYRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 AEAYDVAAIKFRGANAVTNFDISRYDVERIMASS-NLLAGELARRKKDNDPRNKDI--DY 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 DASASRMPGPEYFSNIHYGAGDDRGTEGDFLGSFCLERKIDLTGYIKWWGANKNRQPESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 YWGPGTLINFPVTDYTRDĹBEMONLŚREEYLASĹRRKŚŚĞFŚRGTAKYRGL-----OSRW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 QRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALK 353
                                                                                                  615 FPMPPMETKIVNPIGTSVTSWLPSPTVQMRPSPAISLSHLP 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SKASEDANVEDAGTELKT-LEHTSHATEPYKAPNLGVLCGTORKEKEISSPSSSSALSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 YWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRW 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 KRSSIYRGVTRHRWTGRYEAHLWDKSTWNQNQNKKGKQVYLGAYDDEEAAARAYDLAALK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 SSDQGPKTEAGCSGGGGGSSETVAASDQMLLYRGFKKAKKERGCTAKERISKMPPCTAG
                                                                                                                                                                                                                                                                                                                                                                                         SQSPAFKSLEEKVLKIQE-SCNNENDENANRNIIN----MEKNNGKAIEKPVVSHGVALG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QARIGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AGNKDLYLGTFSTQ------EEA 437
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Nature 402, 761-768, 1999 A;Tittle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: C84686 R;Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, Y.; VanAken, S.B.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999 probable AP2 domain transcription factor [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C; Accession: C84686

A;Cross-references: GB:AE002093; NID:g4510402; PIDN:AAD21489.1; GSPDB:GN00139

Length 464;

371 QLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGT 430 216 DMKQVQNLSKEEFVHILRRQSTGFSRGSSKYRGVTL-HKCGRWEARMGQFLGKKYIYLGL 166 WESHIWD--C---206 TREFSTHQQVLEQQMNCGMGNERNGVSLG-----SVGCGELQSLSLSMSPGSQSSCV 257 h 13.9%; Score 486.5; DB 2; Similarity 35.1%; Pred. No. 1.3e-26; 36; Conservative 55; Mismatches 120; YEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQV 370 ---RNWIDLSFORIGDGETKLVTPVPTPAPVPAQVKKSRRGPRSRSSQYRGVTFYRRTGR 165 TAPSGTDSVAVDAKKRGHAKLGQKQPVH----RKSIDTFGQRTSQYRGVTRHRWTGR 310 TRAFTLSFDILKVGSSSG-GDESPAASASVTKEFFPVSGDCGHLRDVE-----GSSSS-- 108 ---GKQVYLGGFDTAHAAARAYDRAAIKFRGVDADINFTLGDYEE 215 Indels 77; Gaps 274

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APETALA2-like protein Glossy15 - maize
APETALA2-like protein Glossy15 - maize
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T03981
R;Moose, S.P.; Sisco, P.H.
Genes Dev. 10, 3018-3027, 1996
A;Title: Glossy15, an APETALA2-like gene from maize that regulates leaf epidermal cell
A;Reference number: Z15175; MUID:97115883; PMID:8957002
A;Recession: T03981
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: maxNa
A;Residues: 1-446 < cmOO>
A;Cross-references: EMBL:U41466; NID:g1732030; PIDN:AAC49567.1; PID:g1732031
A;Experimental source: strain inbred W64A; leaf
C:Genetics:
A;Gene: Glossy15
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T03981
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indeterminate spikelet 1 - maize
C;Species: Zea mays (maize)
C;Jate: 19-Feb-1999 #sequence_re'
C;Accession: TO1574
R;Chuck, G:; Meeley, R.B.; Hake,
Genes Dev. 12, 1145-1154, 1998
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Best Local Similarity
Matches 119; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPST 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQANGNGSDQKIMNCGNYRNSAFSMALQ 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIDLNLGISLSTGNAPKONGRLFHFPSNTYETORG-VSLRIDNEYMGKPVNTPLPYGSSD 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDSEVEAARAYDKAAINTNGREAVTNFEMSSYONE-INSESN--
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                                                                                                                                                                                                                                                                                                                                                                                                        RRKKDNDPRNKDIDYNKSVVISVMNEETVQVQA---GUNNNENDSEWKMVLFNHPSQQQQ 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMGKKYVYLGLYDTETEÄÄQÄYDKÄÄIKCYGKEÄVTNFDAQSYD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNILAGELA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DINFTLDDYKDEMKKWKDLSKEEFVLVLRRQGAGFVRGSSRFRGVTQ-HKCGKWEARIGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDRRPAAVTQQFFPPTTTAAQQATMEEQCHVPAGSAAEQWVRSSASRKSRRGPRSRSSQY
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                                                                                                                                                                                                      ---AAPDAAPERR 374
                                                                                                                                                                                                                                               SLSSSREASPEKR
                                                                                                                                                                                                                                                                                                                                                                  -KELQSQFWDGELDLELSLGCASSDPSTVAVEAFSPATSSSSRKQRTMTLTLGLFEEEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.8%; ilarity 31.9%; Conservative 7
                                                           #sequence_revision
                                                                                                                                                                                                                                                                                       -YPHPAAGMFGRPADGHVHVAPPPHRQWQQQQQ-GQH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
                         ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --C-----GKÓVYLGGFÓTAQAAARAYDQAAIKFRGLNA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 483; DB 2;
Pred. No. 2.2e-26;
74; Mismatches 114;
                                                                  19-Feb-1999
                                                             #text_change 29-Oct-1999
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A;Title: The control of maize spikelet meristem fate by the APETALA2-like A;Reference number: Z14353; MUID:98221107; PMID:9553044 A;Accession: T01574 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-433 CCUU>
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381 SWAWQAQGSPHVPLHHSAASSGFSTAAGANGGMPLPSHPPAQFP
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                             ----SKIGTHFSNTSSLVTSLSSSREASPEKRGPSLLFP 616
                                                                                                                 DTETEAIDDGDAIDLDLRISQPNVQDPKRDNTL---AGLQPTCDSPESSNTMASQPMSSS
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ce: strain B73
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B; Mismatches 164
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Search completed: March 9, 2004, 10:47:35
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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HYSA STRA3
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3 drosophila
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RESULT 1

ARACHM ATTAMANDARD; PRT; 432 AA.

AD APPLANATH STANDARD; PRT; 442 AA.

AD APPLANATH STANDARD; 
 RC MEDIINE-CV. Columbia;
RX MEDIINE-CV. Columbia;
RX MEDIINE-20083488; PubMed=10617198;
RA Mayer K.F.X., Schweller C., Wambutt R., Murphy G., Volckaert G.,
RA Mayer K.F.X., Schweller C., Wambutt R., Entian K.-D., Terryn N.,
RA Mayer K.F.X., Schweller C., Wambutt R., Rideyer M.,
RA Harris B., Ansorge W., Brandt P., Grivell L.A., Ridger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Wueller M.,
RA Weichselgartner M., puigdomenoch P., Watson M., Schmidtheini T.,
RA Weichselgartner M., Puigdomenoch P., Watson M., Schmidtheini T.,
RA Kreis M., Delseny M., Puigdomenoch P., Watson M., Schmidtheini T.,
RA Kreis M., Delseny M., Puigdomenoch P., Watson M., Schmidtheini T.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Van der Schweren J., Grymonyrez B., Chuang Y.-J., Vandenbussche F.,
RA Van der Schweren J., Grymonyrez B., Chuang Y.-J., Vandenbussche F.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Harzis B., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Hooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Hooijman P., Klein Lankhorst R., Rose M., Lennard N., Dirkse W.,
RA Hootagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Borkova D., Blocker H., Schaerfe M., Grimm M., Duhnerr D., Herzl A.,
RA Mesmann S., Argiriou A., Vitale D., Liguori R., Dauner D., Herzl A.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
Ra Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
Ra Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
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MIX1 CABEL
SPL1 COTUAN
BPEB HUMAN
CYL1 BOVIN
PSU1 YEAST
TF20 MOUSE
FTSX YERPE
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BUD4_YEAST
KINH_LOLPE
SBCC_PSEAE
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Result No.

517 156.5 159.5 139.5 139.5 139.5 134.1 129.5 12

Minimum Maximum

DB 80

seq

Total number of

Scoring

table:

Title: Perfect score:

protein -

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RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante N., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Mattero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lochi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.,
"Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT Thaliana.";
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[3]
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Drews G.N., Bowman J.L., Meyerowitz E.M.;
"Negative regulation of the Arabidopsis h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APETALA2 product.";
Cell 65:991-1002(1991).
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PIR; AB5436; AB5436. 
TRANSFAC; T01774; -. 
InterPro; IPR001471; TF ERF. 
Pfam; PF00847; AP2-domain; 2
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ProDom; PD001423; TF_ERF; 1.
SMART; SMC0380; AP2; 2.
DNA_BIND
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                                                                                                           flowering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shoot apex, and at enhanced levels in the inflorescence meristem, young floral buds, and throughout the early stages of flower development and organogenesis. During floral organ, differentiation it becomes spatially restricted to specific organ, tissue, and cell types within the flower.

INDUCTION: Negatively regulated by the C class floral homeotic protein AGAMOUS in stamens and carpels.

MISCELLANEOUS: Mutations in the APETALA2 gene result in the ectopic expression of AGAMOUS, leading to the replacement of sepals by carpels and stamens and of petals by stamens.

SIMILARITY: Contains 2 AP2/ERF domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUNCTION: Probable transcriptional activator that promotes early floral meristem identity. Is required subsequently for the transition of an inflorescence meristem into a floral meristem. Plays a central role in the specification of floral identity, particulary for the normal development of sepals and petals in the wild-type flower. Acts as A class cadastral protein by repressing the C class floral homeotic gene AGAMOUS in association with others repressors like LEUNIG and SEUSS. It is also required
                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Sepals, petals, stamens, carpels, developing ovules, inflorescence stem, leaf, and stem.

DEVELOPMENTAL STAGE: It is detectable at low levels throughout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          during seed development.
SUBUNIT: May form homodimer.
SUBCELLULAR LOCATION: Nuclear (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402:769-777 (1999).
  Transcription regulation; Activator; Developmental protein; DNA-binding; Repeat.

14 50 ASP/GLU/SER-RICH (ACIDIC; POTENTIAL INVOLVEMENT WITH TRANSCRIPTION).

119 128 NUCLEAR LOCALIZATION SIGNAL (POTENT 128 192 AP2/ERF 1.
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                                                                                                                                                                                                                                                                                                                                                                                            QQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGS-----QSSCVTAPSGTDSVAVD
                                                                                                                                                                                                                                                                                                                                                                                                                  HQTQREEESEEFCYSSPSKRVGSFSNSSSSAVVIEDGSDDDELNRVRPNNPLVTHQFFPE
                                                                                                                                                                                                                                                                                                    ROVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRR
                                                                                                                                                                                                                                                                                                                                             AKKRGHAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKG
                                                                                                                                                                                                                                                                                                                                                                       MDSNGG-----GVASG--
                                                                                                                                                                                                                                    QSTGFPRGSSKYRGVTL-HKCGRWEARMGQFLGKKYVYLGLFDTEVEAARAYDKAAIKCN
                                                                                                                                                                                                                                                KSSGFSRGASTYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAVDVAAIKFR
                                                                                                                                                                                                                                                                              KÓVYLGGFDTAHAAARÁYDRÁAIKFRGVEADÍNÉNÍDDÝDDDLKOMTNLTKEÉFVHVLRR
                                                                           RGPSLLFPMPPMETKIVNPIGTSVTSWLPSPTVQ---
                                                                                                                    VGSGQH-----NMLDESSKIGT--HFS------NTSSLVTSLSSSREASPEK
                                                                                                                                            LSLGNSANS
                                                                                                                                                                  VQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDS
                                                                                                                                                                                          GKDAVTNFDPSIYDEELNAESSG------NPTTPQDHNLD
                                                                                                                                                                                                             GANAVINFDISRYDVERIMASSNLLAGELARRKKDNDPRNKDIDYNKSVVTSVNNEETVQ
                                                                                                                                                                                                                                                                                                                            A----AVVEPAOPL-KKSRRGPRSRSSOYRGVTFYRRTGRWESHIWD
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STANDARD;
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G->E: TEMPERATURE S
G->S: TEMPERATURE S
Q->E: TEMPERATURE S
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Pred. No. 1.4e
56; Mismatches
                                                                                                                                            - KHKSQDMRLRMNQQQQQD
PRT;
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                                                                                                                                                                                                                                                                                                                                                                         -----FPRAHWFGVKFCQSDLATGSSAGKATNVA
248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
.4e-28;
B
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SENSITIVE;
SENSITIVE;
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AP2-1.
AP2-5.
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30-MAY-2000 (Rel. 39, 1
30-MAY-2000 (Rel. 39, I
30-MAY-2000 (Rel. 39, I
Pathogenesis-related ge
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30-MAY-2000
30-MAY-2000
30-MAY-2000
                                                                     Zhou J., Tang X., Martin G.B.;
"The Pto kinase conferring resistance to i
disease interacts with proteins that bind
                                                                                                                                                         Lycopersicon esculentum (Tomato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
lamiids; Solanales; Solanaceae; Solanum.
                      pathogenesis related genes.",
EMBO 7. 16:3207-3218(1997).
-|- FUNCTION: Transcription f.
-|- pathogenesis-related prom
                                                                                                           SEQUENCE FROM N.A.
MEDLINE=97357308; PubMed=9214637;
                                                                                                                                          NCBI_TaxID=4081;
 genes.
SUBUNIT:
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Last
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annotation update)
transcriptional ac
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RESULT 3
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ID SPEN D.
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Best Local S
Matches 47
                                                                                                                                                                                                                                                                                                                                                                                    QSSX\(\overline{\overline{A}}\); QSNHN1; QSNHN1; QSVPL1; QSVPL1; QSVPL2; 10-QCT-2003 (Rel. 42, Created)
10-QCT-2003 (Rel. 42, Last sequence update)
10-QCT-2003 (Rel. 42, Last annotation update)
Spilt ends protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Miscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Nuclear (Probable).
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INTERPRIATE: IPRO01471; TF ERF.

PFINNTS; PR00387; ETHRSPELEMNT.

PRODOM; PD001423; TF ERF; 1.

SMART; SM00380; AP2; -1.
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TRANSFAC; T04717;
                                                                                                                                                             Wiellette E.L., McGinnis W.;
 MEDLINE=20157049; PubMed=10655223; Rebay I., Chen F., Hsiao F., Kolod Suh C., Voas M., Williams A., Rubi
                                                                                                                  to repress the trunk.";
                                                                                                                                                                                                                                            USAGE,
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                            MEDLINE=20025936;
                                                                                                                                                                                                                 TISSUE=Embryo;
                                                                  SEQUENCE FROM
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OR CG18497.
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                                                                                                                                                                                                                                              TISSUE
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ilarity 29.0%;
Conservative 1
                                                                                                   126:5373-5385(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulation; DNA-binding; Activator; Nuclear 95 AP2/ERF.
                                                                  N.A.
                                                                                                                                an RNP motir
e development
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SPECIFICITY, DEVELOPMENTAL
     F., Hsiao F., Kolodziej P.A.,
., Williams A., Rubin G.M.;
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arding K.W., Mace
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Pred. No. 0.00
L6; Mismatches
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mes 54;
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sclerites
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AND MUTANTS I
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SEQUENCE OF 424-2 STRAIN=Berkeley; 'MEDLINE=22426066;

424-2002 FROM N.A. eley; TISSUE=Embryo;

Lewis S.E. Annotation

review

of the Drosophila melanogaster

3:RESEARCH0083.1-RESEARCH0083

.22(2002) euchromatic

genome:

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Sahurner M., Honderson S.N., RA Adams M.D., Celniker S.E., Holt R.A., Sahurner M., Honderson S.N., RA Barandon R.C., Poortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Baris R.G., Blasu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., RA Beseon K.Y., Benos P.V., Berman B.P., Shandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., RA Beseon K.Y., Benos P.V., Berman B.P., Shandari D., Bolshakov S., RA Cherry J.M., Cawley S., Dahlke C., Davrabert L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K., RA Hostin D., Houston K.A., Hewland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kully D., Liai Z., RA Merkulov G., Malshina N.V., Mobarry C., Morris J., Moshrefi A., Renington K.A., Nixon K., Nuzhy L. M., Shues B.C., Siden-Klamos I., Singson M., Skupski M.P., Santh T., RA Shue B.C., Siden-Klamos I., Singson M., Skupski M.P., Smith T., RA Shue B.C., Siden-Klamos I., Singson M., Skupski M.P., Smith T., RA Shue B.C., Singer A., Weinston M., Skupski M.P., Smith T., RA Shue B.C., Siden-Klamos I., Singson M., Skupski M.P., Smith T., RA Shue B.C., Siden-Klamos I., Singson M., Skupski M.P., Smith T., RA Shue B.C., Shapen S., Pan S., Pollard J., Puri V., Reese M.G., Shapen S., Yao Q.A., Wang S., Yao Q.A., Wang S., Yao Q.A., Wang S., Yao Q.A., Wang S., Thu M., Shang S., Zhu X., Smith H.O., RA Shape S., Zhao Q., Zhang L., Zhao Q., Zhang 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=20171275; PubMed=10704397; Kuang B.H., Wu S.C.-Y., Shin Y.-A., Luo L., Kolodziej Kuang B.H., Wu S.C.-Y., Shin Y.-A., Luo L., Kolodziej "split ends encodes large nuclear proteins that regulacell fate and axon extension in the Drosophila embryo Development 127:1517-1529(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase signaling pathway obrosophila identifies split ends, containing protein.";
Genetics 154:695-712(2000).
                                                                                                                                                                   REVISIONS, AND ALTERNATIVE SPLICING.

MEDLINE=22426069, PubMed=12537572,
Misra S., Crosby M.A., Mungall C.J., Malthews B.B., Campbell K.S.

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.

Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.

Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1),
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embryo.";
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Chen F., News,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of putative phosphorylation sites Genetics 155:233-244(2000).
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Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002)
modified entities or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A screen for modifiers of cyclin E functi
melanogaster identifies Cdk2 mutations, re
of putative phosphorylation sites in Cdk2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20253107;
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Lin H.V., Doroquez D.B., Cho S., Chen F., F
"Splits ends is a tissue/promoter specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "split ends, a new component of tregulates development of midline
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                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20414403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION ON
                                                                                                                                            This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event=Alternative promoter;
Comment=2 isoforms, 1 (shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Probable corepressor protein, which regulates different key pathways such as the EGF receptor and Wg pathways. Involved in neuronal cell fate, survival and axon guidance, cell cycle regulation and repression of head identity in the embryonic trunk way act with the Hox gene Deformed and the EGF receptor signaling pathway. Positive regulator of the Wg pathway in larval tissues but not in embryonic tissues. May act as a transcriptional corepressor protein, which repress transcription via the
                                                                                                                                                                  zygotically.
SIMILARITY: Belongs to the Spen family.
SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
SIMILARITY: Contains 1 SPOC domain.
SIMILARITY: Contains 1 SPOC domain.
CAUTION: It is uncertain whether Met-1 or Met-7 is the initiator.
                                                                                                                                                                                                                                                                                                Name=4; Synonyms=SpenS;
IsoId-Q8XS3-4; Sequence=VSP_008565, VSP_008567;
IsoId-Q8XS3-4; Sequence=VSP_008565, VSP_008567;
Note=Produced by alternative splicing of isoform 2;
NISSUE SPECIFICITY: Ubiquitous. Expressed prior to cellularization in stage 3 embryos, and in blastoderm cells, including pole cells. Expressed throughout the rest of embryogenesis. Later, it is expressed at higher level in epidermal cells and CNS.
DEVELOPMENTAL STAGE: Isoform 3 is expressed both maternally and
                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2;
IsOId=Q88X83-2; Sequence=VSP 008565, VSP 008566;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       corepressor protein, recruitment of large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=3; Synonyms=SpenL;
IsoId=Q8SX83-3; Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lopment 130:3125-3135(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q8SX83-3; Sequence=VSP_008567;
Note=Produced by alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q8SX83-1;
  non-profit institutions as and this statement is not remont (no requires a license agreement (no require a license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kebay
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3; PubMed=10959845;
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M., Heidmann D.,
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Kronmiller B., Pacleb
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Nuclear protein; Repeat; RNA-binding; Coiled coil
Alternative promoter usage; Alternative splicing
DOWAIN
554. 632 RNA-BINDING (RRM) 1.
DOWAIN
656 730 RNA-BINDING (RRM) 2.
DOMAIN
734 806 RNA-BINDING (RRM) 3.
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PROSITE; PS00030; RRM RNP_1;
PROSITE; PS50917; SPOC; 1.
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Local Similarity
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AF184612;
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AE003590;
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AAF51535.2;
AAN10511.1;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                        -----FSRGASIYRGVTR----HHQHGRWQARIGRVA
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                                                                                                                                                                                                                            WEDLINE=2254850; PubMed=14593172;

X Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

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"Tennie M., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP23 ARATH STANDARU; rn., 2007.

P42736; O23105;

01-MOV-1995 (Rel. 32, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

AP2 domain transcription factor RAP2.3 (Related to AP2 protein 3)

(Cadmium-induced protein AS30).

AT3G16770 OR MGL6.1 OR MGL6.24.

AT3G16770 OR MGL6.1 OR MGL6.24.
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STRAIN=cv. cc.
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"The AP2 comain or .....";
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proteins in Arabidopsis.";
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Okamuro J.K., Caster B., Villarroel R., van Montagu M., Jofuku K.D.;
"The AP2 domain of APETALA2 defines a large new family of DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S., "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20277480; PubMed=10819329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Columbia;
                                                                                                                               Troukhan M., Alexandrov N., Lu Y.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Columbia;
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Best Local
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EMBL; AF003096; AAC49769.1; -.
EMBL; AB022217; BAB02769.1; -.
EMBL; AY059917; AAL24399.1; -.
EMBL; AY059107; AAK24399.1; -.
EMBL; AY035100; AAK59605.1; -.
EMBL; AY035100; AAK59605.1; -.
EMBL; AY035100; AAK59605.1; -.
EMBL; AY035100; AAK59603.1; -.
EMBL; AY037488; AAM65031.1; -.
HSSP; O80337; 2GCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00380; AP2; 1.
Transcript:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation; DNA-binding; Nuclear protein; Cadmium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSFAC; T02658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: Ref.1 sequence is most probably a cloning artifact and differs from that shown due to an insertion into the sequence.
205 KQQISSLESFLELDGNTAEQPSQLDES 231
                                    555 SAFSMALQDLIGIDSVGSGQHNMLDES 581
                                                                         164 CVV------SQSESE-----LSQPSFPVECIGFGNGDEFQNLSYGFEPDYDL
                                                                                                             500 TSVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSDQKIMNCG-----NYRN
                                                                                                                                                    117
                                                                                                                                                                                         440 AYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKKDNDPRNKDIDYNKSVV 499
                                                                                                                                                                                                                                                                360 RQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAE 439
                                                                                                                                                                                                                                                                                                                                         328 KGRQVYLGGYDMEEKAARAYDLAALKYWG-----PSTHINFSIENYQVQLEEMKNMS 379
                                                                                                                                                                                                                           66 ATEPGKRRKKK-----NVYRGI-RKRPWGKWAAEIRDPRKGVRVWLGTFNTAEEAAM 116
                                                                                                                                                                                                                                                                                                     18 KGRKL----TAEELWSELDASAADDFWGFYSTSKLHPTNQVN-----VKEEAVKKEQ 65
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                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                    AYDVAAKQIRGDKAKLNFPDLHHP---
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         317D50CC514782F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                    --PPPNYTPPPSSPRSTDQPPAKK-----V
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RESULT 5

RAVI_ARATH STANDARD; PRT; 344 AA.

AC Q9ZWM9;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 4), Last sequence update)

DE DNA-binding protein RAVI.

GN RAVI OR ATIG1356 OR TGJ4.2.

OC ENARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Entaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Created by Seguratophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids, OX NCBI_TaxID=3702;

RN SEQUENCE FROM N.A.

RC TISSIE=Seedling;

RX MEDLINE=99081843; PubMed=9862967;
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MEDLINE-22954850; PubMed=14593172;

X Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

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Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

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A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
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WREDLINE-21016719; PubMed=11130712;
White O, Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
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A. M. D., Yu G., Fraser C.M., Venter J.C., Davis R.M.;
Yesquence and analysis of chromosome 1 of the plant Arabidopsis
Thaliana "G., Torion Co."
The All A. M., Mary M. M., Torion C., Mary R.M.;
The All A. M., Mary M., Wenter J.C., Davis R.M.;
The All A. M., Mary M., Wenter J.C., Davis R.M.;
The All A. M., Mary M
                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression in flowers.

DOMAIN: Contains two distinct DNA-binding domains. One is located in the N-terminal region and binds to the 5'-CAACA-3' motif. The second is located in the C-terminal region and binds to the 5'-CACCTG-3' motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ence 302:842-846(2003).
FUNCTION: Binds specifically to bipartite recognition sequences composed of two unrelated motifs, 5'-CAACA-3' and 5'-CACCTG-3'.
SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUE SPECIFICITY: Expressed in all tissues examined: Roots, rosette leaves, cautine leaves, inflorescence stems, flowers an siliques. Highest expression in roots and rosette leaves. Very
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 AP2/ERF domain.
AB013886; I
AC011810; I
AY063855; I
AY091291; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408:816-820(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Columbia;
BAA34250.1; -.
; AAG09554.1; -.
; AAL36211.1; -.
; AAM14230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27:470-478(1999)
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Best Local S
STRAIN=ev. Columbia;

STRAIN=ev. Columbia;

STRAIN=ev. Columbia;

STRAIN=ev. Columbia;

Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,

Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier P.,

Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,

Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

Wincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,

Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,

Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura

Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura

Wiener A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; T51329; T51329.
HSSP; O80337; 2GCC.
InterPro; IPR003340; TF_B3.
InterPro; IPR001471; TF_RRP.
Pfam; PF000447; AP2-domain; 1.
Pfam; PF02362; B3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        O80340;
O80340;
O80340;
O80340;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ethylene responsive element binding factor 4 (Ater4).
Erf4 OR Err4 OR AT3015210 OR K714.1.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                       MEDILINE=20181733; PubMed=10715325;
Fujimoto S.Y., Ohta M., Usui A., Shinshi H., Ohme-Takagi M.;
"Arabidopsis ethylene responsive element binding factors act
transcriptional activators or repressors of GCC box mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERF4_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PRO0367, ETHRSPELEMNT.
PRODOM, PD001423, TF ERF, 1.
DNA-binding, Nuclear protein.
DNA_BIND 59 121 .AI
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      604 ASPEKRGPSLLFPMPPMETKI 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         544 QKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 DNDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 KDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 QRVWLGTFNEEDEAARAYDVAVHRFRRRDAVTNFK----DV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRTLLTSGLSND--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 E
38597 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.0%; Score 141.5; DE 23.4%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B3.
; 7349B640B3505823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .AP2/ERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GVSTTGFRSAEALFEKAVTPSDVGKLNRLVI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      core eudicots; rosids;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KM
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Ra Reichelt J., Scharfe M., Scheen O., Bargues M., Terol J., Climent J.,
Ra Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
Ra Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
Ra Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
Ra Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
Ra Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
Ra Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Ra Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Ra Creasy T.H., Haas B., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
Ra Creasy T.H., Haas B., Walts R., Wu D., Peterson J., Van Aken S.,
Ra Creasy T.H., Haas B., Walts R., Wu D., Peterson J., Van Aken S.,
Ra Creasy T.H., Haas B., Walts R., Wu D., Peterson J., Van Aken S.,
Ra Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
Ra Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
Ra Preuss D., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
Ra Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Watcanabe A., Yamada M., Yasuda M., Tabata S.,
"Gequence and analysis of chromosome 3 of the plant Arabidopsis
Tthaliana.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC; T04636;
InterPro; IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; DNA-binding; Nuclear protein.
DNA_BIND 22 86 AP2/ERF.
DOWAIN 132 137 POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB008106; BAA32421.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Transcription factor that binds to the GCC-box pathogenesis-related promoter element. SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T52019; T52019.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 YRGVTRHHQHGRWQARIGRVAGNKD-LYLGTFSTQEEAAEAYDVAAIKFRGANAVTNF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458 --DISRYDVERIMASSNLLAGELARRKKDNDPRNKDIDYNKSVVTSVNNEETVQVQAGNN 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP000413; BAB02150.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
67; Conserv
                                                                      --PPME 621
                                                                                                                                                                                                                                                                                               GNV-
                                                                                                                                                                                                                                                                                                                                                                                                                                    FLELSDQKVPTGFARSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRGV-RKRPWGRYAAEI-RDPGKKTRVWLGTFDTAEEAARAYDTAARDFRGAKAKTNPPT 82
                                                                                                                                                                                                                                                                                                                                                             NNENDSEWKMYLFNHPSQQQQANGNGSDQKIMNCGNYRNSAFSMALQ-----DLIGIDS 569
                                                                                                                                                                                                                    VGSGQHNMLDESSK------IGTHFSNTSSLVTSLSSSREASPEKRGPSLLFPM- 617
                                                                                                                                             VGRGQPPPVTSAFRSPVVHVATKMACGAQSDSDSSSVVDF----EGGMEKRSQLLDLDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23741 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.0%; Score 139.5; DB 27.2%; Pred. No. 0.0093; tive 22; Mismatches 8
                                                                                                                                                                                                                                                                                               PPQLELSLGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Kauer G., Loehnert T.-H., Nordsiek G.,
Schoen O., Bargues M., Terol J., Climent J.,
Perez-Perez A., Ottenwaelder B., Duchemin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEF16ABA5ACFB073 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SQSSTLDCASPPTLVVPSATA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                                               -GSCYQIPMSRPVYFLDLMGIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                               158
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ID ERF2_ARA/H

AC 080338;

AC 080338;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 41, Last annotation update)

DT 28-FBB-2003 (Rel. 41, Last annotation update)

DE Ethylene responsive element binding factor 2 (AtERF2).

GN ERF2 OR ERF-2 OR AT5647220 OR MQ15.7.

OS Arabidopsis thaliana (Mouse-ear Cress).

OC Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=20181733; PubMed=10715325;
Fujimoto S.Y., Ohta M., Usui A., Shinshi H., Ohme-Takagi
"Arabidopais ethylene responsive element binding factors
transcriptional activators or repressors of GCC box media
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD001423; TF_SMART; SM00380; AP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T04634; -.
InterPro; IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 1
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EMBL; AB018117; BAA97155.1; ~.
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Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; DNA-binding; Nuclear DOMAIN 23 26 POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00367; ETHRSPELEMNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Transcription factor that binds to pathogenesis-related promoter element. SUBCELLULAR LOCATION: Nuclear (Probable). SIMILARITY: Contains 1 AP2/ERF domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T51989; T51989.
                                                                                                                                                                    302 VTRHRWTGRYEAHLWDN-----SCKKEGQTRKGRQVYLGGYDMEEKAAR---AYDLA--A
                                                  352 LKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHG
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68 FHFDTSSSDLSCLFDFPAVKVEPTENFTAMEEKPKKAIPVTETAVKAKHYRGV-RORPWG
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Pred. No. 0.026;
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16-OCT-2004 (Rel. .
15-MAR-2004 (Rel. .
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STRAIN=(57BL/6; TISSUE=Brain;
MEDLINE=99651315; PubMed=9832504;
MEDLINE=99651315; PubMed=9832504;
Garber M.E., Wei P., KewalRamani V.N., Mayall
Rice A.P., Littman D.R., Jones K.A.;
"The interaction between HIV-1 Tat and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99059742; PubMed=9843510;
Blenlasz P.D., Grdina T.A., Bogerd H.P., Cullen B
"Recruitment of a protein complex containing Tat
governs the species specificity of HIV-1 Tat.";
EMBO J. 17:7056-7065(1998).
                                                                                                                         MEDLINE=93145542; PubMed=9990016;
Fujinaga K., Taube R., Wimmer J., Cujec T.P., Peterlin B.M.;
Fujinaga K., Taube R., Wimmer J., Cujec T.P., Peterlin B.M.;
Interactions between human cyclin T, Tat, and the transactivation
response element (TAR) are disrupted by a cysteine to tyrosine
substitution found in mouse cyclin T.";
Proc. Natl. Acad. Sci. U.S.A. 96:1285-1190(1999).
Proc. Natl. Acad. Sci. U.S.A. 96:1285-1290(1999).
Proc. Natl. Acad. Sci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and a critical cysteine residue that is CycTl protein.";
Genes Dev. 12:3512-3527(1998).
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99263519; PubMed=10329126; Kwak Y.T., Ivanov D., Guo J., Nee
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"Role of the human and
                                                                                                                                                                                                                                                                                                                        SSUE=Fibroblast;
                                                       SUBUNIT: Associates with CDK9 to form P-TEPEB predominant cyclin associated with CDK9 (By B: SUBCELLULAR IOCATION: Nuclear (By similarity) SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STR
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SMART; SMUUJBB; CALLEINS; FALSE NEG.
PROSITE; PS00292; CYCLINS; FALSE NEG.
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EMBL; AF109179; AAD13654 1; -.
EMBL; AF087662; AAD17798 1; -.
EMBL; AF113951; AAD17205 1; -.
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LSLDSIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKE LGFELTIDHPHTHVVKCTQLVRASKDLAQTSYFMATNSLHLTTFSLQY RAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGV GL-MSMSTASTSAVPSLPSSEESSSSLTSVD-MLQGERWLSSQPPFKLEAAQ--GHRTSE SISISMSPGSQSSCVTAPSGTDS----VAVDAKKRGHAKLGQKQPVHRKSIDTFGQRTSQ THVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGELQ TVMPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDFLGGATMG-----SRYDVERIMASSNLLAGELARRKKDNDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNEN TRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFR-----GANAVTNFDI ---YRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQ---SGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEKRGP-LSHDSHSSVILKMPIESSE---DSEWKMVLFNHPSQQQQ----ACVCTHLACKWSNWEIPVSTDGKHWWEYV-DATVTLELLDELTHEF------LOILEKTÉSRIKRIRNWRAY-QAAMKTKEDDRG PH-----MKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPL NHHSHRHSHLQLPAGPVSKRPSDPK - KPEEIKMRIKVHSAGDKHNSIEDSVTKSREHKEKORTHPSNHHHHH -ILNMISQTSSDTT-----DHSLQQDGSSAFGSQKQASKSVPSAKVSLKEY----RAK ANGNGSDOKIMNCGNYRNSAFSMALQDLIGIDSVG --NPERPFLDKADKSALKMRLPVASGDKAVSS---QLENMEANVKSQY-VYLGGYDMEEKAA ddl-----THEYGSHERG ----IA -ADENTSEQ -AYAAQNL 122 69 298 242 281 182 241 194 571 520 459 404 395 344 353 297 545 519 474 425

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Matches 137;
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           (CDK9/cyclin T) complex, also called positive transcription elongation factor B (P-TEFB), which is proposed to facilitate the transition from abortive to production elongation by phosphorylating the CTD (carboxy-terminal domain) of the large subunit of RNA polymerase II (RNAP II) (By similarity). Binds also to the transactivation domain of the equine infectious anenia to thrus (EIAV) nuclear transcriptional activator, Tat. It is probably the cis-acting transactivation response element (TAR) RNA binding cofactor for Tat. Does not bind to the transactivation domain of the HIV-1 nuclear transcriptional activator.

SUBCUNIT: Associates with CDK9 to form P-TEFB. Cyclin T1 is the predominant cyclin associated with CDK9 (By similarity).

SIMILARITY: Belongs to the cyclin family. Cyclin C subfamily.
                                                                                     DOMAIN
DOMAIN
                                                                                                                                          SMART; SM00385; CYCLIN; 1.

PROSTTE; PS00282; CYCLINS; FALSE NEG.

Cyclin; Cell cycle; Cell division; Coiled coil;

Transcription regulation; Nuclear protein.

DOMAIN 253 270 NUCLEAR LOCALIZATION SIGNAL

DOMAIN 254 272 TAT:TAR RECOGNITION MOTIF (T
                                                                                                                                                                                                                                            EMBL; AF137509; AAD38518.1; -. InterPro; IPR006670; Cyclin. InterPro; IPR006671; Cyclin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE-9933751; PubMed=10373508; Bieniasz P.D., Grdina T.A., Bogerd H.P., Cullen B.R.; "Highly divergent lentiviral Tat proteins activate viral gene expression by a common mechanism."; Mol. Cell. Biol. 19:4592-4599(1999).

-)- FUNCTION: Regulatory subunit of the cyclin-dependent kinase pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCT1 I
                                                                                                                                                                                                                   Pfam; PF00134; cyclin; 1
SMART; SM00385; CYCLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus
                                                          SEQUENCE
                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
Cyclin T1 (Cyclin T) (CycT1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :SSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HORSE
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSINFPFPPIPTMTQLPGHSSDTSGLPFSQPSCKTR 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SLLFPMPPMETKIVNPIGTSVTSWLP--SPTVQMR 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----HSSQTSTLAHKTYSLSSTLSSS--SSTRKRGPPEETGAAVFDHPAKIAKSTK
   Conservative
                                                          $
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                                                                                        427
528
573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
              3.7%;
                                                          81013 MW;
; Score 129.5; D; Pred. No. 0.26; 80; Mismatches
                                                                                     SIMILARITY).
COILED COIL (POTENTIAL)
POLY-HIS.
POLY-SER.
                                                                          POLY-PRO
                                                           BFC2A398D6B35BCE CRC64;
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                             DB 1;
   221;
   Indels 243;
                             Length
                                                                                                                                                (TRM)
                                                                                                                                                           (POTENTIAL).
Gaps
 31;
   RRRRRRR OCCOORDITA
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            expression.
Plant Cell:
                                                        Fujimoto S.Y., Ohta M., Usui A., Shinshi
"Arabidopsis ethylene responsive element
                                                                                                                                                                                                                                                                                                         ARATH
                                            transcriptional activators or repressors
                                                                                                                              NCBI_TaxID=3702;
                                                                                     MEDLINE=20181733; PubMed=10715325;
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433
                                                                                                                                                                                                                                                                                                                                                                                              635 WLPSPTVQMRPSPAISLSHLP 655
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                 Cell 12:393-404(2000)
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                                                                                                                                                                                                                                                                                                                                                                  FPPLPTMAQLPGHSSDTSGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKADD------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LOILEKTPURLKRIRNWR
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ERF5_ARATH STANDARD; PRT; 300 AA.

080341; Q91VT6;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ethylene responsive element binding factor 5 (AtERF5).
ERF5 OR ERF-5 OR ATSG47230 OR MQL5_9.
                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 HGRWQARIGRVAGNKDLYL-----GTFSTQEEAAEAYDVAAIKFR-----GANAVTNFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 -YRGVTRHRWTGRYEAHLWDNSCKKEG-----QTRKGRQVYLGGYDMEE-KAARAYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 LGFELTIDHPHTHVVKCTQLVRASKDLAQTSYFMATNSLHLTTFSLQY-----TPP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 VV-----ACVCIHLACKWSNWEIPVSTDGKHWWEYV-DATVTLELLDELTHEF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOSLSLSMSPGSQSSCVTAPSGTDSVAVDAKKRGHAKLGQKQPVHRKSIDTFGQRTSQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESSKIGTHESNISSLVISLSSSREASPEKRGP----SLLEPMPPMETKIVNPIGISVIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ASSK--PEEIKMRIKVHAAPDKHNSIDDSVTKSREHKEKHKTHPSNHHHHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SSQTSTLAHKTYSLSSSFSSS--SSSRKRGPPEETGGALFDHPAKIAKSTK--SSSINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SHSSVILKMPIEGSENPERPFLEKPDKTALKMRIPVASGDKA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGS--VGCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVMPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDFLGGATMG-----THEYGSHERG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---DHSLQQDGSNAFTSQKQNSSKSVPSAKVSLKEYRAKHAEEL
H., Ohme-Takagi M.,
binding factors act
of GCC box mediated
                                                                                                                                                                                                                                                                                                            eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----QAAKK
gene
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RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Sakukai T.,

RA Satou M., Tamse R., Vaysberg M., Wallender B.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis

"Genome" "Genome "Genome" "Genome "Genome" "Genome "Genome
                                                                                                                                                                                                                                                                                                        HSSP; O80337; ZGCC.

MR TRANSFAC; T04637; ...

InterPro; TPR001471; TP_ERF.

Pfam; pF00847; APZ-domain; 1.

R PRINTS; pR00367; ETHRSPELEMNT.

ProDom; pD001423; TP_ERF; 1.

SMART; SM00380; APZ; 1.

Transcription regulation; DNA-binding; Nuclear protein.
DNA_BIND 153 218 APZ/FPP
SEQUENCE 200.
                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J., Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J., Hayashizaki Y., Shinozaki K., Arabidopsis thaliana full-length cDNA.", Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

-I-FUNCTION: Transcription factor that binds to the GCC-box pathogenesis-related promoter element.

-i-SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF385709; AAK60301.1; -.
EMBL; AY078014; AAL77715.1; -.
EMBL; AK117568; BAC42229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB008107; BAA32422.1; -.
EMBL; AB018117; BAA97157.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of Arabidopsis thaliana chromosome 5. ) features of the regions of 3,076,755 bp covered by sixty P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20181125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 AP2/ERF domain.
349 LAALKYMGPSTHINFSIENYQVQLEEMKOMSRQEYVAHLRRXSSGFSRGASIYRGVTRHH 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     တ
                                                                                                                                      55
                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20181125; PubMed=10718197; Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Columbia;
                                                                                                                                      Conservative
                                                                                                                                                                           3.7%;
                                                                                                                                 24; Mismatches
                                                                                                                                                                           Score 128.5; DE
Pred. No. 0.084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                      66;
                                                                                                                                                                                                                     Length
                                                                                                                                      Indels
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                                                                                                                                                                                                                         300;
                                                                                                                                      49;
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1 and TAC
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                                                                                                                                 Gaps
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EMBL; M26049; EMBL; Z48612;

AAA34954.1; -. CAA88497.1; -.

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RAD9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDITINE-89313732; PubMed=2664461; Schiestl R.H., Reynolds P., Prakash S., Prakash L.; Cloning and sequence analysis of the Saccharomyces cerevisiae RAD9 gene and further evidence that its product is required for cell cycle arrest induced by DNA damage."; Mol. Cell. Biol. 9:1882-1896(1989).
                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMMI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAD9_YEAST STANDARD; PRT; 1309 AA. P14737; 004920; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                       after DNA damage.";
EMBO J. 17:5679-5688(1998).
-!- FUNCTION: Essential for
following DNA damage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Murphy L., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weinert T.A., Hartwell L.H.;
"Characterization of RAD9 of Saccharomyces cerevisiae and evidence
that its function acts posttranslationally in cell cycle arrest after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEAST
                                                                                                                                                                                                                                                                                                                                                                 Vialard J.E., Gilbert C.S., Green C.M., Lowndes N.F.;
"The budding yeast Rad9 checkpoint protein is subjected to
Mecl/Tell-dependent hyperphosphorylation and interacts with Rad53
                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION, AND INTERACTION WITH RAD53 MEDLINE=98429491; PubMed=9755168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA repair protein RAD9.
RAD9 OR YDR217C OR YD9934.02C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91061763; PubMed=2247073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;

    -!- SIMILARITY: Contains 1 BRCT domain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                               SUBUNIT: Physically associates with RAD53. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 ELCDWDLTGFLNFP 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 NDSEWKMVLF-NHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 PWGKFAAEIRDPNKRGSR-VWLGTFDTAIEAARAYDEAAFRLRGSKAILNFPLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 LPAKTEW-----IQFAAEN--TKPEVTKPVSEEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QHGRWQARI--GRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNEDISRYDVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMASSNLLAGELARRKKDND-PRNKDIDYNKSVVTSV-NNEETVQVQAG-----NNNNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. 10:6554-6564(1990)
                                                                                                                                                                                                                                                                                         cell cycle arrest at the G2 stage X-irradiation or inactivation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KKHYRGV-RQR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466
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Best Local S
Matches 132
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PDB; 1174X; 05-DEC-01.
PDB; 1174X; 05-DEC-01.
PDB; 1174Y; 05-DEC-01.
PDB; 1174P; 05-DEC-01.
PDB; 1174P; 05-DEC-01.
PDB; 1174P; 05-DEC-01.
PDB; 1172N; 05-DEC-01.
PDB; 1174N; 05-DEC-01.
PDB; 1172N; 05-DEC-01.
P
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GO; GO:0005514; C:nucleus; IC.
GO; GO:0005515; F:protein binding; IDA.
GO; GO:0005515; F:protein binding; IDA.
GO; GO:000077; P:DNA damage response, signal transduction re. . .; IMP.
GO; GO:0006289; P:nucleotide-excision repair; IMP.
GO; GO:0006289; P:nucleotide-excision of transcription from P. . .; IMP.
GO; GO:000074; P:prepulation of cell cycle; IGI.
InterPro; IPR001357; BRCT.
Pfam; PP00533; BRCT.
1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation; 3D-structure.

DOMAIN 994 1122 BRCT.

CONFLICT 433 433 C -> S (IN REF. 3).

SEQUENCE 1309 AA; 148413 MW; 6B77D39A95021FB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50172; BRCT; 1.
Cell cycle; DNA damage; DNA replication inhibitor; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                     347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                504 SNSSPIPKEKD------TFNIHEREVETNNVFSNDIONSSNAATRODIIIAGSSDF 553
547 MNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 VPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTVMPLKSDGSLCILEALKRSQTQVMVP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                          RKSMTNVLSPKKHTDDEKDINTHTEVYNNEIESSSEKKEIV-KKDSRDALAEHAGAPSLL
                                                                                                                                                                KFRGANAVTNFDISRYDVERIMASSNILLAGELARRKK---DNDPRNKDIDY
                                                                                                                                                                                                           WIYFETGRSLTKDEDIYYLDIRIGDAVTFDGNEYVVVGLECRSHDLNIIRCIRGYDTVHL 872
                                                                                                                                                                                                                                                   SIY----RGVTRHHQHGRWQARIGRVA---GNKDLYLGTFSTQEE-----AAEAYDVAAI 446
                                                                                                                                                                                                                                                                                          ADNSFLSKDDIIFGNAVWCQYT-WNYKFYPGILLEVDTNQD-----
                                                                                                                                                                                                                                                                                                                                     YDLAALK----YWGPSTHINFSIENYQ----VQLEEMKNMSRQEYVAHLRRKSSGFSRGA 398
                                                                                                                                                                                                                                                                                                                                                                           EENRSTKTSPTKHLKRNSDLDAASIKREPSCSITIQTGETGSGKDSKEQSYVFPE-GIRT 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDGTES--LDVALIEHESKGQSSELQKNLMQLFPSESQEIIQNRRTIKRRQKDTIEIGEE 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSGTDSVAVDAKKRGHAKLGQKQPVHRKSIDTF---GQRTSQYRGVTRHRWTGRYE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLOTSPKKLVVEEETLME--IKKSKGN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGSQSSCVTA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEQKEITDRIYLQLSGKQISDSGSDETERMSPNELDTKKESTIMSEVELTQELPEVEEQQ 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RQQGHMSVQTHPYYSG---LACHGLYQ----APLEEETTKETHVS----DCSSLMPQMTEGL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSS---PKLEDFLGGATMGTHEYGSHERGLSLDSIYYNS-QNAEAQPNRDLL----SQPF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKTQIINSPEQNAL------NATFETPVTLSRINFEPILEVPETSSPSKNTMSKP
                                                                                                                            KKKNASGL----LGKRTLIKALSSISLDLSEWAKRAKIILEDNEKNKGDAYRYLRHPIRG
                                                                                                                                                                                                                                                                                                                                                                                                                    -----GQTRKGRQVYLGGYDMEEKAARA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 103; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRCT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.6%;
18.6%;
                                                                                 TSVNNEETVOVOAGNINNENDSEWKMVLFNHPSOOOOANGNGSDOKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 127.5; D
Pred. No. 0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269; Indels 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLQLHDDNKECNSDK 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                            812
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                                          987
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ATRX PANTR
ID ATRX F
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    밁
  DOMAIN
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Mol. Biol. Evol. 20:1281-1289(2003).

-!- FUNCTION: Could be a global transcriptional regulator. Modifies gene expression by affecting chromatin. May be involved in brain development and facial morphogenesis.
-!- SUBUNIT: Probably binds EZH2. Binds annexin V in a calcium and phosphatidylcholine/phosphatidylserine-dependent manner (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATRX PANTR STANDARD; PRT; 2492 AA.

Q7YQN4;

Q7YQN4;

15-MAR-2004 (Rel. 43, Created)

15-MAR-2004 (Rel. 43, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Transcriptional regulator ATRX (X-linked helicase
                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00271; helicase C
Pfam; PF00176; SNF2 N; I.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interacting with HP1.
-!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
-!- SIMILARITY: Contains 1 PHD-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO01410; DEAD.
InterPro; IPRO01650; Helicase_C.
InterPro; IPRO01330; SNF2 N.
Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitano T., Schwarz C., Nickel B., Paabo S.;
"Gene diversity patterns at 10 X-chromosomal loci in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclear protein) (XNP).
                                                                                                                                                                                                                                                                                                           DNA repair;
Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB102642; BAC81111.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chimpanzees."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22763540; PubMed=12777533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
SUBCELULAR LOCATION: Nuclear, Associated with pericentromeric heterochromatin during interphase and mitosis, probably by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1018
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   1151
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                                                                                                                                                                                                                                                                                                                                          Nuclear
                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                    PHD-TYPE.
                                                POLY-SER.
POLY-LYS.
POLY-SER.
POLY-SER.
POLY-ASP.
POLY-GIU.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                       DNA-binding; Helicase;
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POLY-SER. POLY-LYS.

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RESULT 13

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  MEDLINE=97053827; PubMed=8898241;
Nuckolls G.H., Osherov N., Loomis W.F., Spudich J.A.;
"The Dictyostelium dual-specificity kinase splA is essential for spore differentiation.";
Development 122:3295-3305(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                      protein kinase 1).
SPLA OR PYKA OR DPYK1.
                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Non-receptor tyrosine kinase spore lysis A (EC 2.7.1.112) (Tyrosine-protein kinase 1).
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                                                                                                  STRAIN=JH10
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                             P18160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSRE 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNTKDFDSSEDEKHSKKGMDNQGHKNLKTSQEGSSDDAERK------QERENFSSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFDTKKGKSAKSSIISKKKR----QTQSESSNYDSELEKEIKSMSKIGA---ARTTKKRI 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVE---RIMASSNLLAGELARRKKDND 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-LYDLKTQAGKDDKGKRKKSS-----TSGS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PNKLPKSKQSETVDQ----NSDSDEMLAILKEVSRMSHSSSSDTDINEIHTNHK 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPS-THINFSIENYQ 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAPTREFSTHQQVLEQQMNCGMGNE-----RNGVSLGSVGCGELQSLSLSMSPGSQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRNKDIDYN---KSVVTSVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSD 543
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484 DNDPRNKDIDYNKSVYTSYNNEETYQYQAGNNINIENSEEWKNYLFKHESQQQQANGIGSD 543

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Query Match
Best Local &
Matches 43
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ProDom; PD000001; Prot kinase; 1.

SWART; SW00464; SAM; 1.

SWART; SW00464; SPRY; 3.

SMART; SW00449; SPRY; 3.

SMORT; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00105; SAM_DOMĀIN; 1.

PROSITE; PS50105; SAM_DOMĀIN; 1.
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-! DEVELOPMENTAL STAGE: Expressed throughout development with a peak during the mound stage of morphogenesis.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases.
-!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00069; pkinase; Pfam; PF00536; SAM; 1. Pfam; PF00622; SPRY; 3.
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InterPro; IPR001660; SAM.
InterPro; IPR003167; SPRY_receptor.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS
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EMBL; M33785; AAA33202.1; -.
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SEQUENCE OF 1248-1584 FROM N.A.
MEDLINE=90287147; PubMed=1972546;
Tan J.L., Spudich J.A.;
"Developmentally regulated protein-tyrosine kinase genes"
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN

    -!- FUNCTION: Essential for spore differentiation.
    -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

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       43;
   Similarity 23.9
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                                                                                                                                  AA;
                                                                                                                                                                                                                                 716; splA
                                      23.9%;
                                                                                                                                  174304 MW;
                               3.5%; Score 122;
23.9%; Pred. No. 2.
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Mismatches
                                                                  DB 1; Length 1584;
       86;
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CCT1_PANTR
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                                                                                                       Interro,
Pfam; PFO0134; Cyclin;

R SMART; SM00385; CYCLIN; 1.

R PROSITE; P800292; CYCLINS; FALSE NEG.

W Cyclin; Cell cycle; Cell division; Coiled coil;

W Transcription regulation; Nuclear protein.

TOMAIN 252 269 NUCLEAR LOCALIZATION SIGNAL (POTENT FT DOMAIN 383 424 COILED COIL (POTENTIAL).

TOMAIN 383 424 COILED COIL (POTENTIAL).
Query Match
Best Local S
Matches 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDM9/cyclin T) complex, also called positive transcription (CDM9/cyclin T) complex, also called positive transcription elongation factor B (P-TEYB), which is proposed to facilitate the translition from abortive to production elongation by phosphorylating the CTD (carboxy-terminal domain) of the large subunit of RNA polymerase II (RNAP II). Binds also to the transactivation domain of the HIV-1 nuclear transcriptional activator, Tat. It is probably the cis-acting transactivation response element (TAR) RNA-binding cofactor for Tat. Also serves as an essential cofactor for HIV 2-Tat and similar immunodeficiency virus (African mandrill) Tat function.

1. SUBCUNIT: Associates with CDM9 to form P-TEFB. Cyclin T1 is the predominant cyclin associated with CDM9 (By similarity).

1. SUBCELULLAR LOCATION: Nuclear (By similarity).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=22328476; PubMed=12441807; Rollman E.N., Lund L.H., Sjostrand D.E., Leitner T., Wahren B.F. Rollman E.N., acid deletion in the chimpanzee cyclin Tl does "A unique amino acid deletion in the chimpanzee cyclin Tl does affect Tat trans-activation of HIV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-2004 (Rel.
15-MAR-2004 (Rel.
Cyclin Tl (Cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
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InterPro; IPR006670; Cyclin.
InterPro; IPR006671; Cyclin.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                               TSWLPS-PTVOMRPSPAISLSHL
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AC P25054; Q15162; Q15163;
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DT 01-MAY-1992 (Rel. 22, Created)
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Mammalia; Eutheria;
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"Somatic mutation of th
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    VARIANTS COLORECTAL MEDLINE=98080146; Pu Miyaki M., Nishio J.
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MEDLINE=95135430; Po
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Vogelstein B., Mal
Baba S., Nakamura
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TISSUE=Peripheral blood;

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"The APC variants I1307K and EJ317Q are associated with colorectal tumors, but not always with a family history.";

Proc. Natl. Acad. Sci. U.S.A. 95:10722-10727(1998).
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WEDLINE=98400259; PubMed=9731533;

Wooddage T., King S.M., Wacholder S., Hartge P., Struewing J.P.,

MCAdams M., Laken S.J., Tucker M.A., Brody L.C.;

"The APC II307K allele and cancer risk in a community-based sturn the APC II307K allele and cancer risk in a community-based sturn."
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1 MTNSNNGNGGTNAAAASGWLGFSLSPHMASSTMDEHHHVHHHQQQQQQQQQQQQQHHQ 55	. 4 INESNNIDDGNNHWHLGFSLSPHMKMEATSAATVPTTFYMSPSQSH 49	Query Match 39.1%; Score 1370.5; DB 10; Length 639; Best Local Similarity 46.6%; Pred. No. 1.6e-90; Matches 337; Conservative 68; Mismatches 169; Indels 149; Gaps 30;		SMART; SM00380; AP2; 2.		PRINTS; PR00367; ETHRSPELEMNT.	InterPro; IPR001471; TF ERF.	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	F:transcription factor activity; IEA.	0:0005634;)5309; BAC5	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.	P0474G09.";	sativa nipponbare(., Katayose Y.;	STRAIN=cv. Nipponbare;	SEQUENCE FROM N.A.	[1]		Ehrhartoideae; Oryzeae; Oryza.	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	ď		P0474G09.16.	Putative ovule development protein antitegumenta (ANT).	(TrEMBLrel. 25, Last annotation updat	(TrEMBLrel.	(TrEMBLrel. 24, Creat		Q84Z02 PRELIMINARY; PRT; 639 AA.	л 1 02

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Wing R.A., Yu Y., Soderlund
Saski C., Henry D., Oates R.
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Best Local
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"Rice Genomic Sequence.";

"Rice Genomic Sequence.";

Submitted (DEC-2002) to the EMBL/G

EMBL; AC10389; AAM19141.1; -.

Gramene; Q855W7; -.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005635; P:transcription fa

GO; GO:0003700; F:transcription fa

GO; GO:000475; P: ERF.

Pfam; PF00847; AP2-domain; 2.

PRINTS; PR00367; ETHRSPELEMNT.

ProDom; PD001423; TF_ERF; 2.

SMART; SM00380; AP2; 2.

SMART; SM00380; AP2; 2.

SMART; SM00380; AP2; 2.
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Similarity 47.5%;
33; Conservative 6:
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                                                                                                                                                                               SRYDVERIMASSNILAGELARRKK-----DNDPRNKDIDYNKSVVTSVNNEETVQVQAG
                                                                                                                                                                                                                                      IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDI
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                                                                           VGSGQHNMLDESSKI-GTHFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIVNPI
                                                                                                                                   NNNNENDSEWKKYVLFNHPSQQQQA----NGNGSDQKIMNCGNYRNSAFSMALQDLIGIDS
                                                                                                                                                                                                                   IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFRGLNAVTNFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DPATYYSQGQEAED----ASRAAYQHHQLV---PYN-----YQPLTEAEMLQEAA
                        GTSVTS---WLPSPTVQ----
                                                                                                                                                                  TRYDVDKIMESSSLLPGEAARKVKAIEAAPDHVPIGREL-----GATEBASAATVTG
AVSLAAMNEWMEMPAPAAAHVMREESAI--AHLEVEAAWID
                                                      ESAAADEIDVPGGKISGINFSNSSSLVTSLSNSREGSPERLGLAMLYAKH
                                                                                                          -TDWRMVL--HGSQQQQAAACTEATADLQK-----GFMGDAHS
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Pred. No. 4.3e-88;
2; Mismatches 146;
                MRPSPAISLSHLPVFASWTD
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transcription, DNA-dependent;
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activit;
GO; GO:0006355; P:regulation of transcription,
InterPro; IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 2.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOm; PD001423; TF ERF; 2.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; roside
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (DEC-1995) to
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SPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT
                                                                   KIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREA
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Pred. No. 1.
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SEQUENCE FROM N.A.
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Revan M., Van Der Schueren J.,
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01-NOV-1996
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SEQUENCE FROM N.A.

Chan M.M., Chang C.H., Chang E., Dale J.M., Yamada K., Banh J., Chan M.M., Chang C.H., Chang J.M., Goldsmith A.D., Lee J.M., Onddera C.S., Quach H.L., Deng J.M., Goldsmith M., Mu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Mu H.C., Yamamura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.J. Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou Miranda N., Narusaka M., Shinozaki K., Davis R.W., Ecker Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker
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01-NOV-1996 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sanctation update)
101-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ANT (Putative ovule development protein aintegumenta)
development protein AINTEGUMENTA).
AINTEGUMENTA OR T28119.30 OR AT4G37750.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core euerosids II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL; U4139; AAA91040.1; ...

EMBL; AL0256; AAA91040.1; ...

EMBL; AL055709; CAB38923.1; ...

EMBL; AL055709; CAB38923.1; ...

EMBL; AX1080706; AAL85024.1; ...

EMBL; AX117207; AAM51282.1; ...

PIR; S71365; S71365.

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GO; GO:0006364; C:nucleus; IEA.

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PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF ERF; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                    ----YGEFQQSLSLSMSPGSQSSCITGSHHHQQNQNQNHQSQNH
                                                                                                                                       -VRNTE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1328; DB 10;
Pred. No. 1.5e-87;
9; Mismatches 113;
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transcription, DNA-dependent;
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Best Local S
Matches 263
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GO; GO:000534; C:nucleus; IEA.
GO; GO:0003700; F:transcription f
GO; GO:0003700; F:transcription of t
InterPro; IPR001471; TF_ER:
Pfam; pP00847; AP2-domain; 2.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 2.
SMART; SM00380; AP2; 2.
SEQUENCE 692 AA; 71515 MW; 4D
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Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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Sasaki T., Matsumoto T., Yamamoto
Waryza sativa nipponbare(GA3) geno
clone:P0035F12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV.
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63; Conservative 100;
                                                                                                                                                                                                                                         YQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMN-CGMGNERN
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                                                                                                                                                      KSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFR
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GANAVTNFDISRYDVERIMASSNLLAGELARRKKDNDPRNK-DIDYNKSVVTSVNNEETV
                                                                                                       KSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFR
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71515 MW;
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Pred. No. 1.7e-60;
0; Mismatches 229;
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transcription, DNA-dependent;
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RESULT ID CALES IL ID CALES IL
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R. GO; GO:0005354; C:nucleus; IEA.
R. GO; GO:0006355; P:regulation factor activity; IEA.
R. GO; GO:0006355; P:regulation of transcription, DNA-dependent InterPro; IPR001471; TP_ERF.
R. FORDOM, PR001471; TP_ERF.
R. PINTS; PR00347; AP2-domain; 2.
R. PRINTS; PR00347; AP2-domain; 2.
R. SEARTI, SN00380; AP2; 2.
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Best Local Similarity
Matches 260; Conserv
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01-OCT-2002
01-OCT-2002
01-JUN-2003
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core ev
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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[_TaxID=3702;
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                                                                      MPOMTEGIKNWVAPTRE-FSTHOOVLEQQMNCGMGNERNGVSLG---
                                                                                                                                                                                                                                         VAGGYCFDLAAPSDESSAVQTSFLSPFGVTLEAF----
                                                                                                                                                                                                                                                                                              SDGSLCI-LEALKRSQTQVMVPTSSP---KLEDFLGGATMGTHEYGSHERGLSLDSIYYN
                                                                                                                                                                                                                                                                                                                                                                                                           HUMLGFSLSPHMKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTVMPLK
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                                                                                                                                                                                 SQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKETHVSDCSSL
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nilarity 36.2%;
Conservative 7
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                 ONGPKLENFLGRTTTIYNTNETVVDGNGDCGGGDGGGGGSLGLSMIKTWLSNHSVANA
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 953; DB 10;
Pred. No. 2.2e-60;
5; Mismatches 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1EA3DCDF1C900FB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor activity; IBA.
transcription, DNA-dependent;
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-M., Miki B.L.A.,
                                                                                                                                    NGGACNTL----TINE
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                                                                               Query Ma
Best Loc
Matches
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Boutilier K., Offringa R., Sharma V.K., Kieft H., van l
Boutilier K., Offringa R., Diu C.-M., Miki B.L.,

Zhang L., Hattori J., Ouellet T., Liu C.-M., Miki B.L.,

Custers J.B.M., van Lookeren Campagne M.M.;

"Ectopic expression of the Brassica napus BABY BOOM ger

"Ectopic expression of the Brassica napus BABY BOOM ger

conversion from vegetative to embryonic growth.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ database.

EMBL; AF317905; AAM33801.1;

GO; GO:00056345; P:transcription factor activity; IEA.

GO; GO:00056355; P:regulation of transcription, DNA-dep.
                                                                                                                                                                                            InterPro; IPR001471; TF ERF.
Pfam; PR00847; AP2-domain; 2.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF ERF; 2.
SMART; SM00380; AP2; 2.
SEQUENCE 579 AA; 64018 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002
01-OCT-2002
01-JUN-2003
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Brassica.
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| NHNWLGFSLSP----HKMEATSAATVPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYNARNHYYYAQHQQQQIQQSPGGDFPVAISNNHSSNMYFHGEGGGEGAPTFSVWNDT
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02 (TrEMBLrel. 22, Last sequence update)
03 (TrEMBLrel. 24, Last annotation update)
transcription factor BABY BOOM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                        Conservative
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                                                                                                          27.0%;
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                                                                                                             Score 947;
Pred. No. 5
                                                                                                                                                                                                  6426D3B2B06D3BEA
                                                                                  ore 947; DB 10;
ed. No. 5.9e-60;
Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                               factor activity; IEA.
transcription, DNA-dependent;
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                                                                                                                                                                                                  CRC64;
                          - TEXMS PSOSHLSNEGMCYGV
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                                                                                        Indels
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A Boutiller K., Offringa R., Sharma V.K., Kieft H., van Lammer A Douellet T., Zhang L., Hattori J., Liu C.-M., Miki B.L.A., A Custers J.B.M., van Lookeren Campagne M.M.;

I "Ectopic expression of the Brassica napus BABY BOOM gene tri conversion from vegetative to embryonic growth.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL, AF317904; AAM33800.1; -.

R EMBL, AF317904; AAM33802.1; -.

R GO; GO:0005354; C:nucleus; IEA.

R GO; GO:0005535; P:regulation of transcription, DNA-dependent R GO; GO:000555; P:regulation of transcription, DNA-dependent R InterPro; IPR001471; TF_ERF.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core en
eurosids II; Brassicales; Brassicaceae; Brassica.
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                 STRAIN-cv. Columbia;
MEDLINE=21016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J.
                                                                                                                            SEQUENCE
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5 В δ 밁 Ş 밁 S 밁 Ś В Ś 맑 Ś

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Query Match
Best Local S
Matches 243
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PYODOM; PD001423; TY ERF; 2.
SMART; SM00380; AP2; 2.
SEQUENCE 579 AA; 63962 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHNWLGFSLSP----HMKMEATSAATVPT-----
                                IGTHESNISSLVISLSSSREASPE
                                                                                              S-----QQQQANGNGSDQKIMNCGNYRN-SAFSMALQDLIGIDSVGSGQHNMLDESSK
                                                                                                                                IGSAAKRLKE-----
                                                                                                                                                                  AGELARRKKONDPRNKDIDYNKSVVTSVNNEETVOVQAGNNNNEND---SEWKMVLFNHP
                                                                                                                                                                                                                           ARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLL
                                                                                                                                                                                                                                                                    WGTTTTTNFPMSEYEKEVEEMKHMTRQEYVASLRRKSSGFSRGASIYRGVTRHHQHGRWQ
                                                                                                                                                                                                                                                                                               WGPSTHINFSIENYQVQLEEMKUMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQ
                                                                                                                                                                                                                                                                                                                                   RTSIYRGVTRHRWTGRYEAHLWDNSCKREGQTRKGRQVYLGGYDKEEKAARAYDLAALKY
                                                                                                                                                                                                                                                                                                                                                            RTSQYRGYTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKY
                                                                                                                                                                                                                                                                                                                                                                                                     ----NAAKGLSLSMN--SSTSCDNNNDSNNNVVAQGKTIDDS----VEATPKKTIESFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                 SVGCGELQSLSLSMSPGSQSSCVTAPSGTDSVAVDAKKRGHAKLGQKQPVHRKSIDTFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TIYNTNENV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYGSHERGLSIDSIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYXSGLACHGLYQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVDAFTRDNNSHS-----RDWDINGCACNNIHNDE-----QDGPKLENFLGRTT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GENGNFHSPLTVMPLKSDGSLCILEALKRSQTQVMVFTSSPKLEDFLGGATMGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNNWLGFSLSPYEQNHHRKDVYSSTTTTVVDVAGEYCYDPTAASDESSAIQTSFPSPFGV
                                                                QGVDLSLLHQHQERYNG
                                                                                                                                                                                                  ARIGRVAGNKDLYLGTFGTQEEAAEAYDIAAIKFRGLTAVTNFDMNRYNVKAILESPSLP
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SNTOSLMTNIDHOSSVSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGDGGGGSLGLSM--: IKTW
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                                                                  --YYYNGGNLSSESARACFKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 942; DB
Pred. No. 1.4e:
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EA2AFE4734500D72
 492
                                 607
                                                                                                                                  ANR PVPSMMMISNIVSESENSASGWQNAAVQHH
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.4e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LRNQPVDNVDNQENG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSGCYG----
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Q9CAH3
Q9CAH3;
Q1-JUN-2001 (
01-JUN-2001 (
01-JUN-2003 (
01-JUN-2003 (
F28P22.24
                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; edicotyledons; core et
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                               NCBI_TaxID=3702;
FROM N
                                                                                                                                                                 (TrEMBLrel 17, Created)
(TrEMBLrel 17, Last sequence update)
(TrEMBLrel 24, Last annotation update)
domain transcription factor.
                                                                                                                                                                                                                                                                            PRELIMINARY;
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RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Hunter J.D., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskala I., KwItz D.B., Kwan A., Lam B.,
RA Langin-Hopper S., Lee A., Lee J.M., Linz C.B., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Roomey T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT Williams T., Collon L. C., Collons R. W., Ponter J.C., Davis R. W.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT Thallana.",
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Best Local S
Matches 214
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 2.
PFINTS; PR00367; ETHRSPELEMNT.
PRODOM; PR001423; TF ERF; 2.
SMART; SM00380; AP2; 2.
SMART; SM00380; AP2; 2.
SEQUENCE 425 AA; 48205 MW; C191BA52D6C5ACBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR;
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AC010926; AAG51860.1;
403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLGFSLSPHMKM-----EATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTV
                                                                                                                                                                                                                                                                                                      MPQMTEG-----LKNWV---APTREFSTHQQVLEQQMNCGM---GNERNGVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKETHVSDCSSL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDINFDH-----HHHDEDV-----PKVEDLLS-----NSHQTEYPIN---HN
                                                                                        HQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFRGLNAVTNFDINRYDVKRI
                                                                                                                   HOHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERI
                                                                                                                                                                                   DLAALKYWGPTTHLNFPLSNYEKEIEELNNMNRQEFVAMLRRNSSGFSRGASVYRGVTRH
                                                                                                                                                                                                         SVDSYGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRRGRQAKIGGYDEEEKAARAY
                                                                                                                                                                                                                                                                                                                                                                    NGSM-----LSLALSHGACSDLINESNVSARVEEPVKVDEKRKRLVVKPQVKESVPRK
                                                                                                                                                                                                                                                                                                                                                                                                      -GSVGCGELQSLSLSMSPGSQSSCVTAPSGT----DSVAVDAK-KRGHAKLGQKQPVHRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPNLSNDYGGFERVGSVSVFKSWLEQGTPAFPLSSHYVTEEAGTSNNISHFSNEETGYNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTNVNCTTVVNRLNPP----GYL--
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CSSSTIVDSDQAK
                                              MASSNLLAGELAR
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                                              480
  415
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Pred. No. 1.9e-58;
0; Mismatches 108
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Best Local S
Matches 253
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Gramene; QBLQG3; -
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003701; F:transcription factor activity; IEA.
GO; GO:0003705; F:regulation of transcription, DNA-depen processing proce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8LGQ3;
Q8LGQ3;
Q1-OCT-2002
Q1-OCT-2002
Q1-JUN-2003
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Dukaryche; Viridiplantae; Stre
Spermatophyta; Magmoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BNM3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----MAGGRKEI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGNERNGV$LGSVGCGELQSLSLSMSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÓPÁ-PÓP-AQALSISMNMAGTTTAQGGGAMALLÁGAGERGRTTPASESISTSAHGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGL--YQAPLEEETTKETHVSDCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SD---GSLCILEALKRSQTQVMVPTSSPKLEDFLGGATWGTHEYGSHERGLSLDSIYYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNWLAFSLSPQDQ------LPPSQT-----NSTFISAAATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HNWLGFSLSPHMKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTVMPLK
                                                                                                                                                                                                                                                                                                              FSTQEEAABAYDVAAIKFRGANAVINFDISRYDVERIMASSNLLAGELARRKKDNDPRNK
                                                                                                                                                                                                                                                                                                                                                                                                                                  QLZEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSE-----
                                                                                                                                                                                                                                                                                                                                                                                                  ELEEMKHMTRQEFVASLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEAHLWDNSCRREGOTRKGRO----GGYDKEEKAARAYDLAALKYWGPTTTTNFPVNNYEK
RGWCKQEQDHAVIAAAHSLQDLHHLNLGAAAAAHDFFSQAMQQQHGLGSIDNASLEHSTG
                                                                  ----SQQQQ-----ANGNGSDQKIMNCG--NYRNSAFSMALQDLIGIDSV-----
                                                                                                                                     YDVG---RIASHLGGDGAYAAHYGHHHHSAAAAWPTIAFQAAAAPPPHAAGLYHPYAQPL
                                                                                                                                                                                             (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%;
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22, Last
24, Last
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yta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---NIPQAHP-----STPAIGNGGIGLSMIKNWLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 919.5; DB 1
Pred. No. 6.1e-58;
79; Mismatches 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor activity; IEA.
transcription, DNA-dependent; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GAAAAARKSVDTFGQRTSIYRGVTRHRWTGR
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Query Match
Best Local S
Matches 227
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Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
Ren S.X., Lu G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.,
Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.,
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

BMEL, AL731638; CAED5555.1; -
SEQUENCE 655 AA; 67291 MW; D6FCCD0F729A6933 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q., Hu A., Liu Y.H., Mu J., Yu Z., Shang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.H., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.O., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update
OSJNBA0014K14.16 protein (OSJNBb0116K07.8 protein)
OSJNBA0014K14.16 OR OSJNBB0116K07.8.
OTYZA SALLYA (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pcaceae;
Ehrhartoideae; Oryveae; Oryvea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7X6D4;
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                                                                                                                                               APKLENFLDGNSFSDVHGQAAGGYLYSGSAVGGAGGYSNGGCGGGTIELSMIKTWLRSNQ 173
                                                                                                                                                                                                                                                                                          MPLKSDGSLCILEALKR------SQTQVMVPTS-----
                                                                                                                                                                                                                                                                                                                                           NWLGFSLSGQGNPQHHQNGSPSAA------GDAAIDISGSGDFYGLPTPDAHHIGMA- 56
                                                                                                                                                                                                                                                                                                                                                                                        NWLGFSLS-----PHMKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGAGRMPSWAMTPASAPAATSSSDMTGVCHGAQLFSVWNDT 597
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  MTEGLKNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGSQS
                                                 SQQQP----SPP--QHADQGMSTDASASSYAC-----SDVLVGSCGG----
                                                                                                AEAOPNRDLLSOPFROOGHMSVOTHPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQ 194
                                                                                                                                                                                                 SPKLEDFLGGATM-----GTHEY-----GSHERG-----LSLDSIYYNSQN 134
                                                                                                                                                                                                                                             ---GEDAPYGVMDAFNRGTHETQDWAMRGLDYGGGSSDLSMLVGSSGGGRRTVAGDGVGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTSVTSWLPSPTVOMRPSPAISLSH-----LPVFASWTDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.2%; Score 918.5; DB 10; Length 655; 42.8%; Pred. No. 8.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Mismatches 117; Indels 135;
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Best Local
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Q9LF42;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO1471; TF ERF.
Pfam; PF00847; AP2-domain; 2.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOM; PD001423; TF ERF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL391142; CAC01738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CUN-2003 (TrEMBLrel. 24, Last annotation update)
Ovule development protein aintegumenta-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activit
GO; GO:0006355; P:regulation of transcription,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; T51580; T51580.
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187 DCSSIMPQMTEGIKNWVAPTRE-FSTHQQVILEQQMNCGMGNERNGVSIG-
                                                                                                                        127 SIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKETHVS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413
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                                                                         88 NINNNEQNG-
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                                                                                                                                                                                                                                                                                                                 16 HNWLGFSLSPHMKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTVMPLK 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 08E00MS
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                       VAGGYCFDLAAPSDESSAVQTSFLSPFGVTLEAF-----TRDNNSHSRDWDINGGACN 87
                                                                                                                                                                                                                      SDGSLCI-LEALKRSQTQVMVPTSSP---KLEDFLGGATMGTHEYGSHER-----GLSLD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKHMTRQEYIAHLRRNSSGFSRGASKYRGVTRHHQHGRWQARIGRVAGNKDIYLGTFSTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              64170 MW;
                                                                                                                                                                                                                                                                                                                                                                                     26.2%; Score 916.5; 35.2%; Pred. No. 9.6
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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MEDLINE-99156233; PubMed=10048488;
Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tabata S.,
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OPIT37,
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
similarity to unknown protein.
                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core endicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Sato S., Nakamura Y.,
Submitted (APR-1999)
                                                                            STRAIN=Columbia;
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          638 SPTVQMRPSPAISLSHLPVF 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578 LDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIVNPIGTSVTSWLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 NFPISNYESELEEMKHMTRQEFVASLRRKSSGFSRGASMYRGVTRHHQHGRWQARIGRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 NFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 VTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEBKAARAYDLAALKYWGPSTHI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 NFHSPLTVMPL-KSDGSLCILEALKRSQTQVM-VPTSSPKLEDFLGGATMGTHEYGSHER 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGEL
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                   Kaneko T., Kato T., Asamizu E., To the EMBL/GenBank/DDBJ databases
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Pred. No. 1.3e-56;
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription fa
GO; GO:0006355; P:regulation of tr
InterPro; IPR00471; TF_ERF.
Pfam; PF00847; AP2-domain; 2.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOm; PD001423; TF_ERF; 2.
SWART; SW00380; AP2; 7.
SWART; SW00380; AP2; 7.
SEQUENCE 540 AA; 59066 MW; OAC
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MEDLINE=20277480; I
Nakamura Y.;
"Structural analys
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EMBL; AB
  Q41832;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSY--NTAAFIGNHGIGIGSSSTVGSTEE-----FPTVKTDYDMPSSDGTGGYSGWTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----YNKSV-----VTSVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQ-----
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                                                                                                                                                                                                                              TVOMRPSPAISLSHLPVFASWID
                                                                                                                                                                                                                                                                                                                                                                   LHQQTNNYLQQQSSQN--SQQLYNAYLHSNPAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSRLQLQPYPLSIQQPLEPFLSLQNND---ISHYNNNAHDSS----
                                                                                                                                                                                                                                                                                                                     GTHFSNTSSLVTSL----
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    (TrEMBLrel.
                                                                      PRELIMINARY;
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4; Mismatches
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transcription, DNA-dependent;
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EMBL; Z47554; CAA87634.1; -. PIR; T03638; T03638.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005700; F:transcription ff

GO; GO:0006355; P:regulation of t

InterPro; IPR001471; TF_ERF.
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Orf protein.
ORF.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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ProDom; PD001423; TF_ERF; 2.
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  NNTGSGVMWGATSGAVVGQQDSSSKQGNGYASN
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transcription, DNA-dependent; IEA.
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Abr40851	Abr40762	r4076	r4087	r4085	r4083	r4083	r4082	d3035	083	r4075	r4075	r4076	r4085	r4075	r4083	86050	r4076	r408	r4085
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AC AB Glycine max. Soybean AINTEGUMENTA-like polypeptide GmANT1. 21-OCT-2002 ABB79636; ABB79636 standard; protein; 663 He SS, 21-DEC-2000; 2000US-0257896P. 19-DEC-2001; 2001WO-US049294. 01-AUG-2002. WO200259332-A2 AINTEGUMENTA; ANT-like polypeptide; GmANT1; soybean; transgenic (MONS) MONSANTO TECHNOLOGY LLC Dotson (first entry 3 plant;

New nucleic acids encoding AINTEGUMENTA-like polypeptides useful improving agronomic, horticultural, and quality traits of plants, increased size of plant organs. in such as

WPI; 2002-599798/64. N-PSDB; ABN84480.

Claim 3; Page 130-133; 169pp; English

The present sequence is the protein sequence of GmANT1, a newly identified AINTECUMENTA-like (ANT-like) polypeptide of soybean. The sequence is predicted from clone CPR67663 (see ABN84480), which was obtained from a soybean sequence database screening using Arabidopsis ANT as query. Also isolated was clone CPR67626 encoding GmANT2 (see ABR9637). GmANT1 and GmANT2 show homology to ANT in 2 N-terminal AP2 DNA binding domains, but have C-terminal sequences that bear little, if any, homology to ANT although they share conserved segments with each other. The invention provides nucleic acids encoding ANT-like polypeptides comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding domains followed by an amino acid subsequence selected from those given in ABB79629-35. ANT-like polypeptides have been identified in soybean,

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              Soybean AINTEGUMENTA-like polypeptide
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The present sequence is the protein sequence of GmANT2, a newly condentified AINTGGUMENTA-like (ANT-like) polypeptide of soybean. The consequence is predicted from clone CPR67626 (see ABN84481), which was cobtained from a soybean sequence database screening using Arabidopsis ANT cobtained from a soybean sequence database screening using Arabidopsis ANT comparison, but have C-terminal sequences that bear little, if any, comparison, but have C-terminal sequences that bear little, if any, comparison, in the N-terminal colds encoding ANT-like polypeptides comparising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding comparison, and corn (see ABB79636-41). Nucleic acids encoding the ANT-like polypeptides have been identified in soybean, conton and corn (see ABB79636-41). Nucleic acids (see ABN84480-86) concording the ANT-like polypeptides can be used in the construction of transgenic plants, especially corn, soybean, canola, wheat, cotton, cotton and corn (see ABB79636-41). Nucleic acids (see ABN84480-86) cornotes or potato (all claimed) having improved agronomic, horticultural cornother quality traits, such as increased size of plants organs. These collected from those guence collected from those guence collected from those guence content quality traits, such as increased size of plants organs. These collected from those specially useful for production of ethanol or animal
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Sequence 665
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DB; ABN84481.
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Similarity

49.0%; Score 1715; 54.4%; Pred. No. 7

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Length 665;

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                               H--ESKMIVPHVEENAGESGSIGSMAYGDLQSLSLSMSPSSQSSSVTSSHRASPAVVDSV
                                                                                                                       SGLACHGLYQAPLEEETTKETHVSDCSSLMPQ------MTEGLKNWVAPTREF-STHQ
                                                                                                                                                    GTPHHYECSATETMPLSLDSVFY-IQPSRRDPNNNQTYQNHVQHISTNQQQQQQELQAYY
                                                                                                                                                                                 GT-HEY---GSHERGISIDSIYANSQNAEAQPURDLLSQPFRQ----QGHMSVQTHPYY
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   AVDAKKRGHAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQT
                                                            QVLEQQMNCGMGNERNGV--SLGSVGCGELQSLSLSMSPGSQSSCVT----APSGTDSV
                                                                                           STLRNHDMIL----EGSKQSQTSDNNNLHVQNMGGDDAVPVPGLKSW--EVRNFQASHA
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RESULT 3
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      The present sequence is the protein sequence of OSANT1, a newly identified AINTEGUMENDA-like (ANY-like) polypeptide of rice. The sequence was predicted from a cDNA clone (see AAN94482) obtained from panicle RNA by PCR amplification. OSANT1 cDNA was not amplified from root or leaf RNAs, suggesting tissue-specific expression. Initial OSANT1 clones had been identified in a rice database screening using the newly identified soybean ANT-like polypeptide GMANT1 as query. An additional real ANT-like polypeptide, OSANT1 (see ABB79639), was also isolated. OSANT1 polypeptide shares high homology with Arabidopsis ANT, GMANT1 and GMANT2 at the N-
                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids encoding AINTEGUMENTA-like polypeptides useful in improving agronomic, horticultural, and quality traits of plants, sincreased size of plant organs.
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Best Local Similarity
Matches 341; Conserv
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                                                                 SISSSREASPEKRGPSILFPMPPMETKIVNPIGTSVTS---WLPSPTVQ----MRPSPAI
                                                                                                                                                                                                                                                         LGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKK----
                                                                                                                                                                                                                                                                                                         YRDEIEEMERMTRQEYVAHLRRRSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLY
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                                                                                                                                                                                                                                        LGTFSTQEEAAEAYDIAAIKFRGLNAVTNFDITRYDVDKIMESSSLLPGEAARKVKAIEA
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     SLSHLPVFASWTD
                                     SISNSREGSPERIGLAMIYAKH----
                                                                                                      EATADLQK----GFMGDAHS
                                                                                                                                   NGNGSDOKIMNCGNYRNSAFSMALODLIGIDSVGSGOHNMLDESSKI-GTHFSNTSSLVT
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Pred. No. 2.4e-121;
4; Mismatches 149;
                                                                                                      ALHGIVGFDVESAAADEIDVPGGKISGINFSNSSSLVT
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                                      -HPTAVSLAAMNPWMPMPAPAAAHVMRPPSAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 154-157; 169pp; English.
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Local Similarity 45.3%; Pred. No. 8e-116;
hes 341; Conservative 66; Mismatches 142;
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DB; ABN84483, ABN84484.
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                                                                                                                                                                                                                                                                                                         GGVGGWLGFSLSPHMATYCAGGVDDVGHHHHHHVHQHQQQHGGGLFYNPAAVASSFYYGG
                                                                                                                                                                                                                                                       SQ----SHLSNFGMCYGVGENGNFHSPLTVMPLKSDGSLCILEALK--RSQTQVMVPTSS
                                                                                                                                                                                                                                                                                                                                                           GNNHNWLGFSLSPHMKMEAT-----
GGAVGGDPHHGGGGFLQC--
                                                                                                                                                PKLEDFLG-GATMGTHEYGSHERGLSLD--SIYYNSQNAEAQPNRDLLSQPFRQQGHM-- 154
                                                                                                                                                                                                        GHDAVVTSAAGGGSYYGAG
                                            --SVQTHPYYSG---LACHGLYQAPLEBETTKETHVSDCSSLMPQMTEGLKNWVAPTREF
                                                                                                    PKLEDFLGAGPAM------ALSLDNSAFYYGGHG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry
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                                                                                                                                                                                                           ----FSSMPLKSDGSLCIMEALRGGDQEQQGVVVSAS 129
     -AVIPGAGAG--
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                                                                                                         -----HHQGHAQD
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                                                                                                                                                                                                                                                                                                                                                                                                                         203;
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                                                                                                                                                                                                                                                                                                                                                                   NKDLYLGTF-----STQEEAAEAYDVAAIKFRGANAVTNEDISRYDVERIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPGSQSSCVT---APSGTDSVAVDA--KKRGHA-KLGQKQPVHRKSIDTFGQRTSQYRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRHRWTGRYBAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHIN
NTWASPSPAVSSVPARAGVSIAHLPMFAAWTD
                                     TSWL-PSPTVQMRPSPA-ISLSHLPVFASWID
                                                                                                                     SKIGTHESNISSLVISLSSSREASPEKRGP-----SLLEPMPPMETKIVNPIGTSV
                                                                                                                                                              AAALPAAARTEQQQQHGHGGHQ---HHDLLPSDAFSV-LQDIVSTVDAAGAPPR-----
                                                                                                                                                                                                                                              ESSTLLPGELARRKGKVGDGGG-----AAAVADAAAALVQAG-----NVAEWKMAT
                                                                                                                                                                                                                                                                                                                                NKDLYLGTFIASAFAAARRARHAGTQEEAAEAYDVAAIKFRGLNAVTNFDITRYDVDKIL
                                                                                                                                                                                                                                                                                                                                                                                                             PPLEDYQEELEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                            FSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRHRWTGRYEAHLWDNSCKKEGOTRKGROVYLGGYDMBEKAARAYDLAALKYWGPSTHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAGSQSSCVTVQAAAAGEPYMAMDAVSKKRGGADRAGQKQPVHRKSIDTFGQRTSQYRGV
                                                                                                                                                                                                    ----FNHPSQQQQANGNGSDQXIMNCGNYRNSAFSMALQDLIG-IDSVGSGQHNMLDES
                                                                               TSLGNSREQSPD-RGVGGGGGGGVLATLFAKPAAASKLYSPV--PL
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  899
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AABOT 724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2000
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   WPI; 2000-465969/40
                                                                          Fischer RL,
                                                                                                                                                                                                                              08-JAN-1999;
                                                                                                                                                                                                                                                                                                 07-JAN-2000; 2000WO-US000465
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383. .451
/note= "AP2 domain'
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Query Match
Best Local S
Matches 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an aintegumenta (ANT) polypeptide. The ANT gene is expressed and functions not only in developing ovules but also in various developing organs. Growth and cell proliferation in plant can be modulated by modulating ANT activity. Modulation of ANT activity is used to alter organ mass, control fertility and enhance assexual reproduction in plants. Increased ANT activity can be used to produce male or female sterile plants. Inhibition of ANT activity can be used to truncate vegetative growth, resulting in early flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G---DNTSNFGVCYGSNPNGGIYSHMSVMPLRSDGSLCLMEALNRSSHSNHHQDSSPKVE
                                                                                                                                                                                                                                                                                                                                              DLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPSQSHLSNFGMCYGVGENGNFHSPLTVMPLKSDGSLCILBALKRSQTQVMVPTSSPKLE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKSFCDNDDNNHSNTTNLLGFSLSSNMMKMGGRGGREAIYSSSTSSAATSSSSVPPQLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKRINESNNTDDGNNHNWLGFSLSPH-MKM-------EATSAATVPTTFYM
                                           STPERLLSFPAIFALPOVNOKMFGSNMGGNMSPWTSNPNAELK-TVALTLPOMPVFAAWA
                                                                                        SPEKRGPSL--LFFMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT
                                                                                                                                                                                                  KIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREA
                                                                                                                                                                                                                                                                                                   NDPRNKDIDYNKSVVTSVMNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AENYOKETEDMKNMTROEYVAHLRRKSSGFSRGASTYRGVTRHHOHGRWQARTGRVAGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRWTGRYEAHLWDNSFKKEGHSRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHTNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQISEALVETSVGFETTTMAAAKKKRGQEDVVVVGQKQIVHRKSIDTFGQRTSQYRGVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQMNCGMGNERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTAPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFFG---THHNNTSHKEAMDLSLDSLFYNTTH---EPNTTTNFQEFFSFPQTRNH----
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ilarity 43.5%;
Conservative 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 1328; DB 3; ; Pred. No. 5.8e-114; 69; Mismatches 113;
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                                                                                                                                                      VVEGGSNKEV
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thaliana protein
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              (first
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              entry)
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 fragment
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Protein identification; hybridisation assay; gen genetic signal al transduction pathway; metabolic
mapping; gene expression control; pathway;
promoter;

Arabidopsis thaliana termination sequence

25-FEB 1999 05-MAR 1999 09-MAR 1999 23-MAR 1999 25-MAR 1999 29-MAR 1999 01-APR 1999 01-APR 1999 16-APR 1999 16-APR 1999 16-APR 1999 21 APR-1999
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G---DNTSNFGVCYGSNPNGGIYSHMSVMPLRSDGSLCLMEALNRSSHSNHHQDSSPKVE
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                                                                                                                      69;
                                                                                                                      Score 1328; DB 3;
Pred. No. 5.8e-114;
9; Mismatches 113;
                                                                                                                                                Length
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RESULT 7
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KW CCC
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                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                              transgenic
                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis
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                                                                                                                                                                                           WO2003002751-A2
    (PION-)
                                                                                                           27-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNENDSEWKWVLFNHPSQQQQANGNGSDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLYLGTFGTQEEAAEAYDVAAIKFRGTNAVTNFDITRYDVDRIMSSNTLLSGELARRN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLYLGTFSTQBEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IENYQVQLEEMKUMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STPERLLSFPAIFALPQVNQKMFGSNMGGNMSPWTSNPNAELK-TVALTLPQMPVFAAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AENYQKE I EDMKNMTRQEYVAHLRRKSSGFSRGAS I YRGVTRHHQHGRWQAR I GRVAGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRWTGRYEAHLWDNSFKKEGHSRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GSFNVGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQISEALVETSVGFETTTMAAAKKKRGQEDVVVVGQKQIVHRKSIDTFGQRTSQYRGVTR
                                                                                                                                                                                                                                                                              plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                663
                                                                                                                                                                                                                                                                                                                                                                                                      thaliana oil trait related protein sequence
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      DE NEMOURS & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNSIV--VRNTE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EEET--RNYGND----PSLTHG-
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                                                                                                                                                                                                                                                                                                      inhibition; co-suppression;
                                                                                                                                                                                                                                                                                                                                              MAP kina
kinase;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
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                                                                                                                                                                                                                                                                                                                                                                  kinase;
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Jones
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Novel nucleotide fragment encoding polypeptides protein kinase activity, caleosin-like activity, phenotypes in plants such as sunflower, coconut,
                                                                                                      Tarczynski
 Page 463-465;
                                                                                                      Allen w
Kinney
i MC;
                                                                                                                   ΨB,
                                                                                                                   Cahoon
Klein
542pp;
                                                                                                                    TM,
  English.
                                                                                                                   Epelbaum S, Fan
Li C, Oliveira
                                                                                                                    Famodu OO, Harvira IC, Sakai H,
                           having receptor-like, useful for altering, soybean, wheat and
                                                                                                                                  Harvell LT;
                                                                                                                       Shen
                              rice
                                          011
                                                                                                                       B
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The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIP15-like transcription factor activity and CKC-like activity, ATP citrate lyase activity, NSNT-like cativity and CKC-like transcription factor activity. Also described: (1) cc complement (II) of (I); (2) a chimeric construct (III) comprising (I) or (II), operably linked to a regulatory sequence; (3) a plant (IV) cc comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) cc li obtained from (IV). (I) or its part can be used in antisense coil obtained from (IV). (I) or its part can be used in antisense contained the oil phenotype in a plant such as corn, soybean, wheat, rice, canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 and ABR40591 to ABR40879 represent sequences used in the exemplification of the present

Sequence 555 A

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314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G---DNTSNFGVCYGSNPNGGIYSHMSVMPLRSDGSLCLMEALNRSSHSNHHQDSSPKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPSQSHL$NFGNCYGVGENGNFHSPLTVMPTKSDGSLCILEALKR$QTQVMVPTSSFKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKRINESUNTDDGNNHNWLGFSLSPH-MKM---
                                                                                                                                                                                                                                                                                                                     DFFG----THHNNTSHKEAMDLSLDSLFYNTTH---EPNTTTNFQEFFSFPQTRNH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKSFCDNDDNNHSNTTNLLGFSLSSNMMKMGGRGGREAIYSSSTCSAATSSSSVPPQLVV
                           DLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKKD
                                                                                            IENYQVQLEEMKMMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNK
                                                                                                                                                                     HRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFS
                                                                                                                                                                                                                   QQISEALVETSVGFETTTMAAAKKKRGQEDVVVVVGQKQIVHRKSIDTFGQRTSQYRGVTR
                                                                                                                                                                                                                                              THPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE
                                                                                                                                              HRWTGRYEAHLWDNSFKKEGHSRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFS
DLYLGTFGTQEEAAEAYDVAAIKFRGTNAVTNFDITRYDVDRIMSSNTLLSGELARRN--
                                                                     AENYOKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                              -GSFNVGV
                                                                     BDMKNMTRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.9%;
                                                                                                                                                                                                                                                                                              ---YGEFQQSLSLSMSPGSQSSCITGSHHHQQNQNQNQNHQSQNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1328; DB 6;
Pred. No. 5.8e-114;
9; Mismatches 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            555;
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The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIP15-like transcription factor activity and CKC-like transcription factor activity and CKC-like transcription factor activity. Also described: (1) CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or CC complement (II) in its genome; (4) sequence; (3) a plant (IV) CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) CC inhibition or co-suppression in a transformed plant. (III) is useful for CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice, CC canola, Brassica, sorghum, sunflower or coconutt. (III) is also useful for CC creating transgenic plants having altered lipid profiles. (I) can also be CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor caleosin; ATP citrate Lyase; SNF1; CKC-like transcription factor; antisense inhibition; co-suppression; transgenic plant.
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Jones
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08-JAN-1999; 07-JAN-2000;

VINU

WO200040694-A2

mass,

Modulating

Claim 15;

Page

556

465

501 919 496

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asexual reproduction; early flowering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an aintegumenta (ANT) polypeptide. The ANT gene is expressed and functions not only in developing ovules but also in various developing organs. Growth and cell proliferation in plant can be modulated by modulating ANT activity. Modulation of ANT activity is used to alter organ mass, control fertility and enhance asexual reproduction in plants. Increased ANT activity can be used to produce male or female sterile plants. Inhibition of ANT activity can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fischer RL, Mizukami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   truncate vegetative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ating growth and cell proliferation in a plant used to alter organ
control fertility and enhance asexual reproduction in plants
ises modulating ANT activity and selecting plants with altered cel
                                                                                                                                                                                                                                                                                                                                                                                                                                 9 NTDDGNNHNWLGFSLSPHM-----KMEATSAATVPTTFYMSPSQ----SHLSNFGMCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                              TMGTHEYG-SHERG--LSLDSIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLA
                                                                                                                                                                                                                                                                                                                                                                       GVG-ENGNFHSPLTVMPLKSDGSLCILEALKRS------QTQVMVPTSSPKLEDFLGGA
                                                                                                                                                                                                                                                                                                                                                                                                      DNDDSNTTNLLGFSLSSNMLKMGGGEALYSSSSSSVATS--SVPPQLVVGDNSSNYGVCY
                        ROEYVAHLRRKSSGFSRGASIYRGVTRHHOHGRWQARIGRVAGNKDLYLGTFSTQEEAAB
                                                                           CKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNWS
                                                                                                             TTTMAAAAAKKKRGQEVVVGQKQIVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNS
                                                                                                                                 SGTDSVAVDAKKRG-HAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNS
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                                                                                                                                                                                                                              ------EEET--RNYEND-----PGLTHG-----
                                                                                                                                                                                                                                                     CHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGN
                                                                                                                                                                                                                                                                                         -FGTHHHNTSHKEAMDLSLDSLFYNTTHA---PNNNTNFQEF----FSFPQTRNHH----
                                                                                                                                                                                                                                                                                                                                              GSNLAAREMYSQMSVMPLRSDGSLCLMEALNRSSHSNNHHHSQV----
RQEYVAHLRRKTSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAE
                                                       FKKEGHSRKGROVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFSVENYOKEIDDMKNMT
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05-MAR-1999;
09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment
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                                                                                     Protein identification; signal transduction pathway; metabolic
hybridisation assay; genetic mapping; gene expression control;
termination sequence.
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                     EP1033405-A2
                                                     Arabidopsis thaliana
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Pred. No. 5.6e.
63; Mismatches
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les 102;
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Best Local Simi
Matches 301;
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RWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASS
                                            TQVMVPTSSPKLEDFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF
                                                                                                                                                                           QQNQNQNHQSQNHQQISEALVETSVGFETTTMAAAKKKRGQEDVVVVGQKQIVHRKSIDT
                                                                                                                                                                                                                                            -----GSFNVGV-----YGEFQQSLSLSMSPGSQSSCITGSHHH
                                                                                                                                                                                                                                                               PTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTAPS--
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Llarity 44.6%;
Conservative 6;
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S-01577589

S-01577589

S-01584589

S-015877589

S-01589329

S-01589329

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S-016893379

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Pred. No. 5.7e-111;
3; Mismatches 102;
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                         The present sequence is the protein sequence of GhANT1, a newly cidentified AINTEGUMENTA-like (ANT-like) polypeptide of cotton. The sequence was predicted from a cDNA clone (see ABN94485) isolated in a cotton DNA database screening. The invention provides nucleic acids cencoding ANT-like polypeptides comprising, in N-terminal to C-terminal cideraction, 2 AP2 DNA binding domains followed by an amino acid subsequence selected from those given in ABB79629-35. ANT-like polypeptides were identified in soybean, rice, cotton and corn (see ABB79636-41). Nucleic acids (see ABN94480-86) encoding the ANT-like polypeptides can be used in the construction of transgenic plants, ceapecially corn, soybean, canola, wheat, cotton, tomato or potato (all traits, such as increased size of plant organs. These plants are cespecially useful for production of ethanol or animal feedstuff
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-2002
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                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                             New nucleic acids encoding AINTEGUMENTA-like polypeptides useful in improving agronomic, horticultural, and quality traits of plants, such as
                                                                                                                                                                                                                                                                                                                       WPI; 2002-599798/64.
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size of plant organs.
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                                                                               DSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIVNP
                                                                                                                                   AGNNNNE-NDSEWKWYLFNHPSQQQ-QANGNGSDQKIMNCGNYRNSAFSMALQDLIGI--
                                                                                                                                                                                        NAVTNEDISRYDVERIMASSNILAGELARRKKONDERNKDIDYNKSVVTSVNNEETVQVQ
                                                                                                                                                                                                                       SGFSRGASVYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFRGT
                                                                                                                                                                                                                                              SGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGA
                                                                                                                                                                                                                                                                             VYLGGYDKEEKAAKAYDLAALKYWGPTTHINFPLSTYEKELEEMKNWTRQEFVAHLRRKS
                                                                                                                                                                                                                                                                                          VYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKS
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 LGN---
                          IGTSVTSWLPSPTVQMRPSPAISLSH-LPVFASWTD
                                                                                                          SGEASDELADMVWTA---NSDEQQQHQSTNTNNDASLANSSS-RNSSNPQSPKGSIGLAS
                                                                                                                                                                  SAVTNEDISRYDVKRICSSSTLIGGELAKRSPKDTASIAPEDYN-SCASSASPQPLLAIP
                                                                                                                                                                                                                                                                                                                                  KRPVGKNLTRESVPRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQ
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                                                      -GDYSHHG-YFSLKGSKYEDGNSETDNSNENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GLSLDSIYYNSQNAEAQPN-----
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  -LGLVHKIPMFALWNE
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Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; IJP15-like transcription factor caleosin; ATP citrate lyase; SNF1; CKC-like transcription factor; antisense inhibition; co-suppression;
             09-JAN-2003
                                                                                transgenic plant
                                                                                                                                                          Glycine max oil trait related protein sequence
                                                                                                                                                                                 16-MAY-2003
                                                                                                                                                                                                                                ABR40856 standard; protein;
                                    WO2003002751-A2
                                                          Glycine
                                                                                                                                                                                                          ABR40856;
                                                            max.
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SEQ

ID NO:491

Query Match Best Local

Local Similarity

33.7%;

Score 1180.5; DB 5; Pred. No. 3.4e-100;

Length

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                                                                    유 성
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Matches
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Jones
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DB; ACC00850.
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VVTSVNNEETVQVQAGNNNNE-NDSEWKMVLFNHPSQQQQANGNGSDQKIMNCGNYRNSA
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Kinney AJ,
i MC;
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llarity 43.1%;
Conservative 6
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Klein
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Pred. No. 3.8e-
67; Mismatches
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Li C, Oliveira IC, Sakai H, Shen B;
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3.8e-89;
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    The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIPIS-like transcription factor activity and CKC-like transcription factor activity and CKC-like transcription factor activity. Also described: (1) cc complement (II) of (I); (2) a chimeric construct (III) comprising (I) or CC (II), operably linked to a regulatory sequence; (3) a plant (IV) CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) coll obtained from (IV). (I) or its part can be used in antisense collection or co-suppression in a transformed plant. (III) is useful for CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice, canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00888 and ABR40591 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor like protein kinase; mitogen activated profein Lipp5-like transcription factor calessin; ATP ottrate ly CKC-like transcription factor; antisense inhibition: cotransgenic plant.
                                                                                                                                                                                                                                                                   Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering phenotypes in plants such as sunflower, coconut, soybean, wheat and a
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N-PSDB; ACC00803.
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PIONEER
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Li C, Oliveira IC,
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Sakai H, Sl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASTEYMFPAQPVLAGGGGGSNSSNTSNSSSIGLSM---IKTWL---RNQPPHSENNNN
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                                                                                                                                                                                                                                                PEKRGPSLLFPMPPMETKIV-----
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                                                                                                                                                                                                                                                                                                                                                                               VAAIKFRGLSAVTNFDMSRYDVKSILESTTLPIGGAAKRLKDMEQVELRVENVHRADQED
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  trait;
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  oil phenotype; altered lipid
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Pred. No. 8.8e-89;
4; Mismatches 203
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                            protein sequence SEQ ID NO:352
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QQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGSQSSCVTAPSGTDSVAVDAKKRGHAK

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The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC polypeptide (PP) having receptor-like protein kinase activity, mitogen CC activated protein (MAP)-kinase activity, LIPIS-like transcription factor contribution factor contribution factor activity and CKC-like transcription factor activity. SNF1-like CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or CC comprising (III) in its genome; (4) sequence; (3) a plant (IV); and (5) CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) CC collobtained from (V). (I) or its part can be used in antisense CC contibition or co-suppression in a transformed plant. (III) is useful for CC campla, Brassica, sorghum, sunflower or coconut. (III) is also useful for CC creating transgenic plants having altered lipid profiles. (I) can also be CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to invention
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Jones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering phenotypes in plants such as sunflower, coconut, soybean, wheat and phenotypes in plants such as sunflower, coconut, soybean, wheat and provided the such as sunflower, coconut, soybean, wheat and provided the such as sunflower, coconut, soybean, wheat and provided the such as sunflower, coconut, soybean, wheat and provided the such as suc
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N-PSDB; ACC00801.
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NSASTDYMFPAQPVSAGGGGSGGSNNNNNSNSIGLSM---IKTWL-----RNQPPNS
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Kinney AJ,
WC;
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Klein TM,
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                                                                                                                                                                                                                                                                                                                                                                                                              88;
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Pred. No. 1.4e-
88; Mismatches
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Li C, Oliveira IC, Sakai H, Shen
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	LYYLTQQQSSSVDTVKASAYDQGSACNTWVPTAIPTHAPRSTTSMALCH 696	648	Дb
	RGPSLLFPMPDMETKIVNPIGTSVTSWLPSPTVQMRPSPAISLSH 653	609	Ş
647	YGGGGYNVMPMGTTTAVVASDGDQNPRSNHGFGDNEIKALGYESVYGSATDSYHAHARN 647	588	В
809	GSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEK 608	571	Ş
587	QQDNSDAPHSLSYSDIHQLQLGNNGTHNFFHTNSGLHPMLSMDSASIDNSSSSNSVVYDG	528	9
570	QQANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSV	535	Ş
527	DHSIIMSSHLTQGINNNYAGGGTATHHNWHNAHAFHQPQPCTTMHYPYGQRINWCKQE	470	В
534	DYNKSVVTSVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQ	493	Ś
469	DVAAIKFRGLSAVTNFDMSRYDVKSILESTTLPIGGAAKRLKDMEQVELSVDNGHRADQV	410	ф
492	DVAAIKFRGANAVINFDISRYDVERIMASSNILAGELARRKKDNDFRNKDI 492	442	Ś
409	EYVASLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAY 409	350	g
441	EYVAHLRKKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEBAAEAY	382	8
349	REGOTRKGROVYLGGYDKEEKAARAYDLAALKYMGTTTTTNFPISHYEKELEEMKHMTRO	290	g
381	KEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENTQVQLEEMKNMSRQ	322	Ş
289	SDNKQPNTSAALDSTQTGAIETAPRKSIDTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCR	230	д
321	LGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCK	278	Ş
229	ENINNNNESGGNIRSSVQQTLSLSMSTGSQSS-TSLPLLTASVDNGESS 229	182	뮍

Search completed: March 9, 2004, 10:45:34 Job time: 63 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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      US-09-227-421-2
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US-08-912-272-10
US-08-912-272-10
US-08-912-272-11
US-08-912-272-11
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US-08-912-272-5
US-08-912-272-7
US-08-912-272-7
US-08-912-272-7
US-08-912-272-7
US-09-198-119C-52
US-09-198-119C-53
US-09-198-119C-71
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Sequence 3, Appli
Sequence 87, Appli
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Patent No. 6559357
Patent No. 6559357
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Feri
TITLE OF INVENTION: and Enhancing Assexual Reproduction in Plants
TITLE OF INVENTION and Enhancing Assexual Reproduction in Plants
CURRENT APPLICATION NUMBER: US/09/227,421
CURRENT APPLICATION NUMBER: US/09/227,421
PRIOR APPLICATION NUMBER: US/09/227,421
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH; 555
TYPE: PRT
CRGANISM: Arabidopsis thaliana
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US-09-227-421-2
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Sequence 57, Appl	e 59	Sequence 4, Appli	•	, App	e 69, App	•	e 29,	e 29,	e 93,	e 77,	equence 34,	`	e 27,		Seguence 83, Appl	, App	•

## ALIGNMENTS

Controlling Fertility

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Query Match
Best Local Similarity
Matches 314; Conserv
230 QQISEALVETSVGFETTTMAAAKKKRGQEDVVVVGQKQIVHRKSIDTFGQRTSQYRGVTR
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                                                              -----GTDSVAVDAKKRGH---AKLGQKQPVHRKSIDTFGQRTSQYRGVTR
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APPLICANT: Fischer, Robert L.
APPLICANT: Fischer, Robert L.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
FILE REFERENCE: 023070-090720US
CURRENT APPLICATION UNMERR: US/09/479,855
CURRENT FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 555
TYDE. DOT
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Best Local Similarity
Matches 314; Conserv
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                                                                                                                                                                                                                                                                       DFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKRINESNNTDDGNNHNWLGFSLSPH-MKM------EATSAATVPTTFYM
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   QQMNCGMGNERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTAPS----
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                                                                                                                                   THPYYSGLACHGLYQAPLESETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE 217
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Pred. No. 3.4e-123;
9; Mismatches 113;
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; ORGANISM: Brassica napus
US-09-227-421-5
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US-09-227-421-5
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SEQ ID NO 5
LENGTH: 548
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Patent No. 6559357

GRMERRAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling
TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
                                                                                                                                                                                                                   Query Match

Best Local Similarity 43.6%;
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 023070-090700PC
CURRENT APPLICATION NUMBER: US/09/227,421
CURRENT FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: US 09/227,421
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 8
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                                                                                                                            DNDDSNTTNILGFSLSSNMLKMGGGEALYSSSSSSVATS--SVPPQLVVGDNSSNYGVCY
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                                                       GSNLAAREMYSOMSVMPLRSDGSLCLMEALNRSSHSNNHHHSOV---
                                                                                          GVG-ENGNFHSPLTVMPLKSDGSLCILEALKRS-----QTQVMVPTSSPKLEDFLGGA 109
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                                                                                                                                                                                                Score 1307; DB 4; Length 548; Pred. No. 4.1e-121; 7; Mismatches 103; Indels 22
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Sequence 5, Application US/09479855

Patent No. 6639128

GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
FILE REFERENCE: 023070-090720US
CURRENT APPLICATION MUMBER: US/09/479,855
CURRENT FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 548
TYPE: PRT
ORGANISM: Brassica napus
OTHER INFORMATION: cannola AINTEGUMENTA (ANT)
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                                                                                                                                   NTDDGNNHNWLGFSLSPHM-----KMEATSAATVFTTFYMSPSQ----SHLSNFGMCY
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                      GSNLAAREMYSOMSVMPLRSDGSLCLMEALNRSSHSNNHHHSQV----SSPKMEDF----
                                                  GVG-ENGNFHSPLTVMPLKSDGSLCILEALKRS------QTQVMVPTSSPKLEDFLGGA 109
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                                                                                               DNDDSNTTNLLGFSLSSNMLKMGGGEALYSSSSSSVATS--SVPPQLVVGDNSSNYGVCY
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, 43.6%; Pre-
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                                                                                                                                                                        Score 1307; DB 4;
Pred. No. 4.1e-121;
7; Mismatches 103;
                                                                                                                                                                                                          Length 548;
                                                                                                                                                                          Indels 220;
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US-08-700-152A-4
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Patent No. 5994622
GENERAL INFORMATION:
APPLICANT: Jothuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for
COUNTRY; USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,152A
FILING DATE: 20-AUG-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067200US
TELECHONNE: (415) 576-0300
TELEPHAN: (415) 576-0300
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ADDRESSEE: Townsend and Townsend
STREET: Two Embarcadero Center, E
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                                                                                                                                                                                                                                                                                                                                              STREET: Two Embarca
CITY: San Francisco
STATE: California
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US-08-912-272-9
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                                                                                                                                                                                                                                                                                                                              ; Sequence 9, Application
; Patent No. 6093874
; GENERAL INFORMATION:
APPLICANT: Jofuku,
APPLICANT: Okamuro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 163; Conserv
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                                                 ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                  APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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FILING DATE:
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGS-----QSSCVTAPSGTDSVAVD 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOTOREESEEFCYSSPSKRVGSFSNSSSSAVVIEDGSDDDELNRVRPNNPLVTHOFFPE
                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08912272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- HNQIFNSTSTPHQNWLQTNGFQPPLMRPS 432
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                  US/08/912,272
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Best Local S
Matches 69
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                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,039
FILING DATE: 19-FEB-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US 08/912,272
FILING DATE: 15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09026039 Patent No. 6329567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 20-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 20-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 20-JUN-1997
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Methods for Improving CONTRESPONDENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jofuku, F
APPLICANT: Okamuro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Region LOCATION: 44..59 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                          STREET: Two Embarcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 GPSTHINFSIENYOVQL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
69; Conserv
                                                                                                                                                                                                                                   94111-3834
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ilarity 89.6%;
Conservative
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Okamuro, Jack K.
ÆNTION: Methods
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alpha-helix (SEQ ID NO:37)"
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Pred. No. le-30;
3; Mismatches
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                                                                                                                                                                                                                                                                                                             Eighth Floor
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 20-UUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
APPLICATION NUMBER: US 01

US 08/879,827

US 08/700,152

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Best Local Similarity 89.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08912272 Patent No. 6093874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: PR PC TOOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Region
LOCATION: 44..59
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jofuku, K. Diane APPLICANT: Okamuro, Jack K.
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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                                                                                    APPLICATION NUMBER: FILING DATE: 15-AUC
                                                                                                                                                                                                                                                                                                                                                                                      PLICANT: Okamuro, Jack K.
TLE OF INVENTION: Methods for Improving Seeds
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                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                           94111-3834
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                                                                                        15-AUG-1997
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alpha-helix (SEQ ID NO:37)"
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                                                                                                             US/08/912,272
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Pred. No. 1e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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US-09-026-039-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/09026039
Patent No. 6329567
GENERAL INFORMATION:
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                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PSECHLIN Release #1.0, Ve.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/026,039

FILING DATE: 19-FEB-1998

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,272

FILING DATE: 15-AUG-1997

PRIOR APPLICATION DATA:

APPLIC
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INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
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LENGTH: 69 amino acids
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APPLICATION NUMBER: US 0 FILING DATE: 20-JUN-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 103
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LOCATION: 37..51
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..69
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Embarca
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 9.9%; Local Similarity 94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
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Two Embarcadero Center, E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methods for Improving Seeds 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "putative ANT-R2 amphipathic
alpha-helix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "ANT-R2 direct repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0300
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                                                                        US 08/879,827
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Pred. No. 6.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d and Crew LLP
Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                     Version
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US-08-700-152A-1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Applic
Patent No. 5994622
                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
CYCTEM: PC-DOS/MS-DOS
TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
ITILE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
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TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                          ATTORNEY/ACENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LOCATION: 37..51
OTHER INFORMATION:
OTHER INFORMATION:
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 20-AUG-1996
CLASSIFICATION: 800
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LOCATION: 1..69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08700152A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%;
llarity 94.2%;
Conservative
  (415) 576-0300
DR SEQ ID NO: 1:
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alpha-helix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "ANT-R2 direct repeat"
                                                                                                                                                                                          US/08/700,152A
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                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/912,272
APPLICATION NUMBER: US/08/912,272
FILING DATE: 15-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUM-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/700,152
FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Form Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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STREET:
SITY: San Franction California
TNTE: California
TISA
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
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CORRESPONDENCE ADDRESS:
Townsend and Townsend
STREET: Two Embarcadero Center, E
                                                                                                                                                         REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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                                                                                                    SEQUENCE CHARACTERISTICS:
MOLECULE TYPE:
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Local Similarity 51.9%; Pred. No. 4.5e-12;
nes 40; Conservative 12; Mismatches 15
                                                                                                                                                                                                                  NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                  TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
                 TOPOLOGY:
                                                                            ENGTH:
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                                                       amino acid
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                                                                            67 amino acids
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                 linear
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Eighth Floor
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RESULT 12
US-09-026-039-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                   TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
                                                                                                                                                                                                        APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-UTN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/700,152
PILING DATE: 20-AUG-1996
ATTORNEY/ACENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 15-AUG-1997 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/912,272
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving
                                                                                                                                                     NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Region LOCATION: 33..49 OTHER INFORMATION: OTHER INFORMATION:
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarca
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/026,039
                               STRANDEDNESS:
                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 TSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYW 355
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                                                  amino acid
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                                                                                                                                        576-0200
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alpha helix (SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "RAP2.7-R1 direct repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 192.5; DB 3;
Pred. No. 1.3e-11;
                                                                                                                                                                           023070-067230US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKOVYLGGFDTAHAAARAYDRAAIKFR 50
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RESULT 13
US-08-700-152A-2
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Patent No. 5994622
GENERAL INFORMATION:
APPLICANT: Jofuku,
APPLICANT: Okamuro
                                                                      US-08-700-152A-2
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Query Match 5.1
Best Local Similarity 60.1
Matches 41; Conservative
                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 68 amino acids TYPE: amino acid
                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 20-AUG-1996
                                                                                                                                                                                                                                                                                                                             NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKST NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                  LOCATION: 1..68
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                   MOLECULE TYPE:
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 TSQYRGVTRHRWTGRYBAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYW 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 GPSTHINFSIENYQVQLEEM 375
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Two Embarcadero Center, Eighth Floor
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Okamuro, Jack K.
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                                                                                                                                                                                                                       linear
                                                                                                                                                                     Domain
                                                                                                                                                                                                     peptide
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                   60.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methods for Improving Seeds
                                                                                 /note= "APETALA 2 (AP2) of Arabidopsis direct repeat domain AP2-R2 consisting of amino acids 221-288 of the AP2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "putative RAP2.7-R1 amphipathic
alpha helix (SEQ ID NO:36)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "RAP2.7-R1 direct repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 192.5; DB 4;
Pred. No. 1.3e-11;
                                                                                                                                                                                                                                                                                                                                                                         023070-067200US
     Score 191.5; DB 2
Pred. No. 1.6e-11;
8; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GKOVYLGGFDTAHAAARAYDRAAIKFR 50
                                     DB 2;
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                                     Length
                                        68;
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US-08-912-272-5
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                                                                                                                                        US-08-912-272-5
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bastian, Kevin L.
REFERENCE/DOCKET NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
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                                                                                             Query Match
                                                                                                                                                       PEATURE:
NAME/KEY: Region
LOCATION: 33..50
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JOIUKU, ... APPLICANT: Okamuro, Jack K.
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
PRIOR APPLICATION DATA:
US 08/879,827
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 20-JUN-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 15-AU
                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
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458 DISRYDVE 465
                                                          ch 5.5%; Score 191.5; DB 3; Length 68; 1 Similarity 60.3%; Pred. No. 1.6e-11; 41; Conservative 8; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
                                                                                                                                                                                                                                                                                                                                                                                                                          68 amino acids
                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                             peptide
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                                                                                                                                                       /note= "putative AP2-R2 amphipathic
alpha-helix (SEQ ID NO:7)"
                                                                                                                                                                                                                                                    /note= "AP2-R2 direct repeat at
positions 221 to 288"
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                                                                                                Query Match
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                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 20-UUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
ETIING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 15-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                       NAME/KEY: Region LOCATION: 33..50 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                        LOCATION: 1.68
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
                                                                             Local Similarity 60.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME:
                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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398 ASIYRGYTRHHQHGRWQARIGRVAGNKDLYLGIFSTQEEAAEAYDVAAIKFRGANAVTNF 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458 DISRYDVE 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415)
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                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                         /note= "putative AP2-R2 amphipathic
alpha-helix (SEQ ID NO:7)"
                                                                                                5.5%;
                                                                                                                                                                                                                                                        /note= "AP2-R2 direct repeat at positions 221 to 288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 08/700,152
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                                                            8; Mismatches
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                                                        Score 191.5; DB 4; Length 68; Pred. No. 1.6e-11; B; Mismatches 18; Indels
                                                        1; Gaps
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458 DISRYDVE 465 | | | | | 60 DPSIYDEE 67

Search completed: March 9, 2004, 10:48:10 Job time: 25 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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-Q=/Cgn2 1/USPTO_spco1/US10024632/runat_09032004_101208_10797/app_query.fasta_1.839
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-DSV _TIMEOUT=30 -THREADS=1 -XGAPDS=10 -XGAPEXT=0.5 -FGAPOP=6
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## ALIGNMENTS

Sequence 1, Application US/09227421 Patent No. 6559357

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GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
TITLE OF INVENTION: And Enhancing Asexual Reproduction in Plants
FILE REFERENCE: 023070-990700PC
CURRENT FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: US/09/227,421
PRIOR APPLICATION NUMBER: US/09/227,421
PRIOR APPLICATION NUMBER: US/09/227,421
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LEMOTH: 2148
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (1269).. (1336)
OTHER INFORMATION: AINTEGUMENTA (ANT)
NAME/KEY: misc feature
LOCATION: (1309).. (1339)
OTHER INFORMATION: encodes first AP2 domain
NAME/KEY: misc feature
LOCATION: (1404).. (1414)
OTHER INFORMATION: encodes linker region
NAME/KEY: misc feature
LOCATION: (1405).. (1521)
OTHER INFORMATION: encodes second AP2 domain
US-09-227-421-1
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Qy  1 MetlysArgIleAsmGluSerAsmAsmThrAspAspGlyAsmAsmHisAsmTrpLeuGly 20	Alignment Scores:  Pred. No.:  \$1328.00	Oy  1814 ATGTTCGGATCAAATATGGGCGGAAATATGAGTCCTTGGACATCAAACCCTAATGCTGAG  OY  643 MetAigProSerProAlalleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp 662  1874 CTTAAGACCGTCGCTCTTGCCTCAGATGCCGGTTTTCGCTGAT  OY  663 Thr 663  Db 1931 TCT 1933  RESULT 2  US-09-479-855-1  Sequence 1, Application US/09479855  Patent No. 6639128  GENERAL INFORMATION: Methods for Altering Organ Mass, Controlling Fertility FIITLE OF INVENTION, Mothods for Altering Organ Mass, Controlling Fertility FIITLE OF INVENTION, Mothods for Altering Organ Mass, Controlling Fertility FIILE REPERENCE: 023070-009720US  FILE REPERENCE: 023070-009720US  FILE ROPE INVENTION NUMBER: US/09/479,855  CURRENT FILING DATE: 2000-01-07  NUMBER OF SEQ LD NOS: 8  SOFTWARE: Patentin Ver. 2.1  LENGTH: 2148  FEATURE: OTHER INFORMATION: AINTEGUMENTA (ANT) CDNA  NAME/KEY: CDS  INCATION: (269)(1936)  COTHER INFORMATION: AINTEGUMENTA (ANT)  US-09-479-855-1
306 1139 326 1199 346 1259 366 1319 406 1439	Qy 269 AspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHis 285	

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RESULT 3
US-09-227-421-4
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Patent No. 6559357
GENERAL INFORMATION:
                                                                SEQ ID NO 4
LENGTH: 1738
                                                                                           APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling
FILER OF INVENTION: and Enhancing Assaual Reproduction in Plants
FILER PAPPLICATION NUMBER: US/09/227,421
CURRENT FILING DATE: 1999-01-08
FRIOR APPLICATION NUMBER: US 09/227,421
PRIOR PILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
ORGANISM: Brassica FEATURE: NAME/KEY: CDS
                                                TYPE: DNA
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Best Local Similarity:
Query Match:
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; Patent No. 6639128
; GENERAL INPORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass, Contro
TITLE OF INVENTION: and Enhancing Asexual Reproduction in
FILE REFERENCE: 0230770-090720US
CURRENT APPLICATION NUMBER: US/09/479,855
CURRENT APPLICATION NUMBER: US/09/479,855
CURRENT FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 1738
TYPE: DNA
ORGANISM: Brassica napus
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Best Local Similarity:
Query Match:
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; LOCATION: (1)..(1647)
COTHER INFORMATION: canola AINTEGUMANTA
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                                                                                                                                                                                                                                                                                                                                                                                     16 GATAATGATGATAGTAATACGACTAATTTGCTAGGGTTCTCGTTGTCTTCAAATATGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTTTCGCTGCGTGGGCTGATTCT 1644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuProSerProThrValGlnMetArgProSerProAlaIleSerLeuSerHisLeuPro
    CATAGTCAAGTT-
                                                                                                            AspGlySerLeuCysIleLeuGluAlaLeuLysArgSer-----
                                                                                                                                                         ĠĠŤŦĊŦĂĄĊŦŦĄĠĊĄĠĊŦĄĠĠĠĄĄĄŦĠŦĄŤĊŤĊĄĄĄŦĠŦĊŦĠŤĠĄŤĠĊĊĊĊŦĊĄĠĄŦĊŦ
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                                         GlnThrGlnValMetValProThrSerSerProLysLeuGluAspPheLeuGlyGlyAla 109
                                                                                                                                                                                          GlyValGly---GluAsnGlyAsnPheHisSerProLeuThrValMetProLeuLysSer
                                                                                                                                                                                                                                   ---TCTGTTCCÁCCACÁGCTTGTTGTTGGCGACAACAGTÁGCÁÁCTATGGÁGTTTGCTÁC
                                                                                                                                                                                                                                                                        TyrMetSerProSerGln-----SerHisLeuSerAsnPheGlyMetCysTyr
                                                                                                                                                                                                                                                                                                                                                    GACGGTTCTCTTTGCTTAATGGAAGCTCTCAACAGATCTTCTCACTCGAATAATCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.01e-128
1307.00
54.52%
43.50%
37.32%
      TCATCTCCAAAGATGGAAGATTTC
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Matches:
Conservative:
Mismatches:
Indels:
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8 멍 Ş 밁

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309 89 249 76 189 57 132 41

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluArgAsnGlyValSerLeuGlySerValGlyCysGlyGluLeuGlnSerLeuSerLeu 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspCysSerSerLeuMetProGlnMetThrGluGlyLeuLysAsnTrpValAlaProThr 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysHisGlyLeuTyrGlnAlaProLeuGluGluGluThrThrLysGluThrHisValSer 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProPheArgGlnGlnGlyHisMetSerValGlnThrHisProTyrTyrSerGlyLeuAla 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||::::::||||||||:::
AGTTTATTCTACAATACCACTCATGCG------CCAAACAACAACAACACCAACTTTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyThrAspSerValAlaValAspAlaLysLysArgGly---HisAlaLysLeuGlyGln 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTCAAAACCACCAGCAGATCTCTGAAGCTTTGGTCGAGACAAGTGCTGGATTTGAGACA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgGluPheSerThrHisGlnGlnValLeuGluGlnGlnMetAsnCysGlyMetGlyAsn 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----AGAAACTACGAGAAT
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                                                                                                                                                                                                                                                                       ACTAATTTCTCTGTGGAGAATTATCAGAAAGAGATTGATGACATGAAGAACATGACTGA
                                                                                                                                                                                                                                                                                                IleAsnPheSerIleGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArg
                                                                                                                                                                                                                                                                                                                                                                                   GluLysAlaAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHis 360
                                                                                                                                                                                                                                                                                                                                                                                                                               AGAAGGAAGGTCATAGCAGAAAAGGAAGACAAGTTTATCTGGGGGGTTATGATATGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGTTACAAGACATAGATGGACTGGTAGGTATGAAGCTCATCTATGGGACAATAGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyValThrArgHisArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCys 320
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                                                                TyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgVal
                                                                                                                                                                                            CAAGAATATGTTGCTCACTTGAGAAGAAAAACCAGTGGTTTCTCTAGGGGTGCTTCCATC
                                                                                                                                                                                                                            GlnGluTyrValAlaHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIle
                                                                                                                                                                                                                                                                                                                                                  GAGAAAGCTGCTCGAGCATATGATCTTGCTGCACTCAAGTACTGGGGTCCCTCTACTCAC
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TyrAspValAlaAlaIleLysPheArgGlyAlaAsnAlaValThrAsnPheAspIleSer 460
                                                                                                                    TATAGAGGAGTCACCAGACATCACCAGCATGGAAGGTGGCAAGCTCGGATCGGTAGAGTC
                                         GCTGGAAACAAAGATCTCTACCTTGGAACTTTCGGAACTCAAGAAGAAGCGGCGGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TTTAGCTTCCCTCAAACTAGAAACCACCAT-------
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정 음 성 음

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1621 GTTTTCGCTGCGTGGATTCT 1644	В
656 ValPheAlaSerTrpThrAspThr 663	Qy
1564 ACTACGAACCCTAATGCTGATCTCAAGACCGTTTCTCTTACTCTGCCGCAGATGCCG 1620	В
636 LeuProSerProThrValGlnMetArgProSerProAlaIleSerLeuSerHisLeuPro 655	8
1507 CCTCAAGTTGGTCCGAAGATGTTCGGAGCAAATGTGGTCGGAAATATGAGTTCTTGG 1563	망
618 ProProMetGluThrLysIleValAsnProIleGlyThrSerValThrSerTrp 635	λδ
1489CCGACGATATTTGCGTTG 1506	Дb
598 LeuSerSerArgGluAlaSerProGluLy8ArgGlyProSerLeuLeuPheProMet 617	γQ
1488 1488	DЬ
578 LeuAspGluSerSerLysIleGlyThrHisPheSerAsnThrSerSerLeuValThrSer 597	ş
1488 1488	망
558 SerMetAlaLeuGlnAspLeuTleGlyTleAspSerValGlySerGlyGlnHisAsnMet 577	δ
1462GGTAGCCCGGAGAGGGTTTTGAGTTTT	g
538 AsnGlyAsnGlySerAspGlnLysIleMetAsnCysGlyAsnTyrArgAsnSerAlaPhe 557	δ
1459 GTG 1461	ф
518 GluAsnAspSerGluTrpLysMetValLeuPheAsnHisProSerGlnGlnGlnGlnAla 537	Q
1399 AACATTAGCGACGAGGÁAGCCGCTTTAÁCCGCTGTCGTGAACGGTGGTTCCAÁTAAGGAA 1458	망
501 SerValAsnAsnGluGluThrValGlnValGlnAlaGlyAsnAsnAsnAsn 517	Qy
1372 AGGAACAGCAÁCAGCATCGTGGTCCGC 1398	В
481 ArgLysLysAspAsnAspProArgAsnLysAspIleAspTyrAsnLysSerValValThr 500	88
1312 AGGTACGATGTTGATCGCATAATGGCTAGTAACACTCTCTTGTCTGGAGAGATGGCTCGA 1371	Ф
461 ArgTyrAspValGluArgIleMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArg 480	γQ
1252 TATGATGTAGCAGCTATCAAGTTCCGTGGCACAAACGCGGTGACTAACTTTGACATAACA 1311	ρb

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RESULT 5
US-08-700-152A-3
US-08-700-152A-3
; Sequence 3, Application US/08700152A
; Patent No. 5994622
; Patent No. 5994622
; Patent No. 5994622
; APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DATE: 1EM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION: 800
ATTORNEY/AGENT INFORMATION:

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-024-632-2 (1-663) x US-08-700-152A-3 (1-1680)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 190..148
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCAAACACAAAGAAAAAAATCTGAAGAGTTTTGTTATTCTTCACCAAGTAAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrGlnAlaProLeuGluGluGluThrThrLysGluThrHis-----
                                                                                                                                                                                                                                                      AspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHisArgTrpThrGly 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGATTCTAACGGCGGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGAACTTAACCGGGTCAGACCCAATAACCCACTTGTCACCCATCAGTTCTTCCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTGGATCTTTCTCTAATTCAAGCTCTTCAGCTGTTGTTATCGAAGATGGATCCGATGAC
                                           AlaAlaLeulysTyrTrpGlyProSerThrHisIleAsnPheSerIleGluAsnTyrGln
                                                                                                                                                                                  ArgTyrGluAlaHisLeuTrpAspAsnSerCysLysLysGluGlyGlnThrArgLysGly 329
                                                                                                                                                                                                                                                                                                                                AlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHisArgLysSerIle 289
                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCACTGGTTTGGTGTTAAGTTTTGT---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnGlnMetAsnCysGlyMetGlyAsnGluArgAsnGlyValSer-----
               GCTGCTATTAAATTCCGTGGAGTAGAAGCGGATATCAATTTCAACATCGACGATTATGAT
                                                                                  AAACAAGTTTACTTAGGTGGATTTGACACTGCTCATGCAGCAGCTCGAGCATATGATAGA 705
                                                                                                         ArgGînValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaArgAlaTyrAspLeu 349
;;;||||||||||||||||||
                                                                                                                                                          AGATGGGAATCTCATATTTGGGAC----TGT
                                                                                                                                                                                                                            CGTGGACCAAGATCAAGAAGTTCTCAGTATAGAGGTGTTACGTTTTACCGGCGTACCGGA
                                                                                                                                                                                                                                                                                                                                                                                                    proGlySerGlnSerSerCysValThrAlaProSerGlyThrAspSerValAlaValAsp 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1488
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517.00
43.76%
31.29%
14.76%
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                                                                                                                                                                                                                                                                                                                                                                     CAGTCGGATCTAGCCACCGGATCGTCCGCGGGTAAAGCTACCAACGTTGCC
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                                                                                                                                                                                                                                                                                                - GCCGTAGTGGAGCCGGCACAGCCGTTG---AAAAAGAGTCGG
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Mismatches:
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; Sequence 3, Application US/09026039
PATENT NO. 6329567
; GENERAL INFORMATION:
APPLICANT: Jofuku, K. Diane
; APPLICANT: Ocamuro, Jack K.
TITLE OF INVENTION: Methods for IT
NUMBER OF SEQUENCES: 103
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REGISTRATION NUMBER: 34,774
REFERENCE DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/
FILING DATE: 20-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
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MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
COMPUTER: LEM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/026,039
FILING DATE: 19-FEB-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,272
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
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LOCATION:
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 11721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                         1166 TTCACCAAGTAAACGGGTTGGATCTTTCTCTAATTCTAGCTCTTCAGCTGTTGTTATCGA 122
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                                                                                                                                              2106 AĞCACAĞĞCTTCCCTCĞAĞĞAAGTTCĞAAĞTATAĞAĞĞTĞTCACTTTG---CATAAGTGT 2162
                                                                                                                                                                                                                           2046 TGAATTTTATAGATGACTAATTTAACCAAGGAAGAGTTCGTACACGTACTTCGCCGACAA 210s
                                                                                                                                                                                                                                                                                                        1986 TATAAACTATATTGGTTTTTATTAACGATTTTTAAAGGTTTGGGAGATTAATATTGAAAT 2045
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                                                                                                                                                                                 391 SerSerGlyPheSerArgGlyAlaSerIleTyrArgGlyValThrArgHisHisGlnHis 410
                                                                                                                                                                                                                                                                                                                                                                                                                              359 ThrHisileAsnPheSerileGluAsnTyrGlnValGlnLeuGluGlu-------
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                                                                                                  411 GlyArgTrpGlnAlaArgIleGlyArgValAlaGly-----
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                                                               ĠĠŦĊĠŦŦĠĠĠAĄĠĊŦĊĠĀAŦĠĠĠŦĊAAŦŦĊŦŦAĠĠĊAAAAĠŦAŦĀAŦŦŦĊŦĊŦĊAŦŦŦŦ 2222
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	SOFTWARE: PatentIn Release #1.0, Version #1.30  CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/026,039  FILING DATB: 19-FEB-1998  CLASSIFICATION: 800  PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/912,272  FILING DATE: 15-AUG-1997  PRIOR APPLICATION NUMBER: US 08/932,272  FILING DATE: 20-JUN-1997  PRIOR APPLICATION NUMBER: US 08/879,827  FILING DATE: 20-JUN-1997  PRIOR APPLICATION NUMBER: US 08/879,827  FILING DATE: 20-JUN-1997  APPLICATION NUMBER: US 08/700,152  FILING DATE: 20-AUG-1996  ATTORNEY/AGENT INFORMATION: NAME: Bastian, Kevin L.	proving Seed and Crew LL Eighth Floor	Db 2223 ATATTCACTCGAAAACTTCATTTTAGTTTGTTATTTTAACTTTGAGTTTTTGTTTTCTTG 2282  Qy 423
Qy  319	Qy 244 uSerLeuSerMetSerProGlySerGlnSerSerCysValThrAlabroSerGlyThrAs 264  Db 10351	YLEUTYTGINALAPTOLEUGIUGIUGIUTHTTHILYSGIUTHTHIS	CTHER INFORMATION: /note= "Arabidopsis APETALA2 (AP2)  CHER INFORMATION: genomic sequence"  US-09-026-039-3  Alignment Scores:

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                              APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNOCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT FILING DATE: 199-05-14
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 6727
LENGTH: 301
TYPE: DNA
CURNITSM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6727, Application US/09313294A Patent No. 6476212 GENERAL INFORMATION:
NAME/KEY: misc_feature
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                                                                                                                                                                                                    TITLE OF INVENTION. Plant Having Altered Environmental Stress Tolerance FILE REFERENCE: 1917,713 Seq List CURRENT APPLICATION NUMBER: US/09/198,119C CURRENT FILING DATE: 1998-11-23 PRIOR APPLICATION NUMBER: US 08/706,270 PRIOR FILING DATE: 1998-02-03 PRIOR NUMBER: US 09/018,235 PRIOR APPLICATION NUMBER: US 09/018,235 PRIOR PRIOR PRIOR DATE: 1998-02-03 PRIOR PRIOR PRIOR DATE: 1998-02-03 PRIOR DATE: 1998-02-03 PRIOR PRIOR PRIOR DATE: 1998-02-03 PRIOR PRIOR PRIOR DATE: 1998-02-03 PRIOR PRIOR DATE: 1998-02-03 PRIOR PRIOR PRIOR DATE: 1998-02-03 PRIOR 
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                                                                                                                        SOFTWARE: Pa
SEQ ID NO 54
LENGTH: 898
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APPLICANT:
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OTHER INFORMATION: a, t, c, g, or other
                                                     ORGANISM: Brassica napus
   OTHER INFORMATION: bnCBF5 gene
                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
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Gilmour, Sarah
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Conservative:
Mismatches:
Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Sequence 6, Application Patent No. 6653533 GENERAL INFORMATION:
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                                                                                                              LysIleMetAsnCysGlyAsnTyrArgAsnSerAlaPhe
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APPLICANT: Purdue Research Foundation
ITILE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
FILE REFERENCE: 7024-371
CURRENT APPLICATION NUMBER: US/09/202,161B
CURRENT FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: CCT/US97/10382
PRIOR APPLICATION NUMBER: 607/046,494
PRIOR APPLICATION NUMBER: 60/046,494
PRIOR APPLICATION NUMBER: 60/019,633
PRIOR FILING DATE: 1997-05-14
PRIOR APPLICATION UNMER: 60/019,633
PRIOR FILING DATE: 1996-06-12
NUMBER: OF SEQ ID NOS: 30
SOFTWARE: ASCII
SEQ ID NOS: 30
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Best Local Similarity:
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Sequence 1, Application Patent No. 6329567
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GENERAL INFORMATION:
APPLICANT: Jofuku,
APPLICANT: Okamurc
TITLE OF INVENTION:

T: Jofuku, K. Diane T: Okamuro, Jack K. INVENTION: Methods

Jack K. Methods

for

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RESULT 12	Db 1661 CACT 1664	Qy 404 lThr 405	Db 1601 GCATGTCATTÄGÄÄGGCAAÄGCACTGGGTTTCCAAGÄGGCAGCTCTAAGTÄTÄGÄGGTGT 1660	Qy 384 lAlaHisLeuArgArgLyBSerSerGlyPheSerArgGlyAlaSerIleTyrArgGlyVa 404	Db 1541 CGAACATAAAACAAATTAATATTTGTTGCAGATGACGCAGTTGACAAAGGAAGAGTTCAT 1600	777	Qy 371 nLeugluglumethys	1421	Qy 351 aLeuLysTyrTrpGlyProSerThrHisIleAsnPheSerIleGluAsnTyrGlnValG1 371		Qy 343AlaAlaArg-AlaTyrAspLeuAlaAl 351	Db 1301 TTTTACTCATCCAAATATGATCAATTAGAACGAATCTAATATTCCTTATTTTGTAATTTC 1360	Oy 336GlyTyrAspMetGluGluLys	Db 1241 TATTACTTTTGTTACATATTCAGGTGGATTTGACACAGCACATGCCGCTGCTCGGTATG 1300	Оу 335 335	Db 1181 TTGTGTCTGTCCATTTTTATATGATTTCTTCGACCAAATAAAGGTTTTATTATCTCCTTA 1240	Qy 335 335	Db 1121 GTATGATCATGTAATGTTGTTCAAACACAGATCAAATATCCTATTGAAACTAAGTTGTG 1180	Qy 335 G1y 335		317	_	Oy 316 316	Db 942 TGGGAGTCACATATTTGGTAACTTAATTTTCTTAACCCGACGATATACCGAATACTATTA 1001	311 TyrGlijAlaHisLeiTrp	Qy 291 ThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgH1sAtgTrpThrGlyArg 310		Qy 271 LysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHisArgLysSerIleAsp 290	Db 786 AGAAACCAGTCTTGTTCGGTCGAATCCTAGCGGGTCTGGT 827	Qy 251 GlySerGlnSerSerCysValThrAlaProSerGlyThrAspSerValAlaValAspAla 270	Db 753785	231	TCCGAATCAAATCATGGAACAG	211

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FILLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance;
FILE REFERENCE: 19117.713 Seq List
CURRENT APPLICATION NUMBER: US/09/198,119C
CURRENT FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: US 08/706,270
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/017,575
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,227
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,227
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,227
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; Patent No. 6417428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jiang, (TITLE OF INVENTION: FILE REFERENCE: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-02-03
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495 AsnLysSerValValThrSerValAsnAsnGluGlu---
                                                                                                                                                                                     464 ValGluArgIleMetAla----------SerSerAsnLeuLeu 474
                                                                                                                                                                                                                                   407 TCGGCTTGGCCGCTCCGTATCCCGGAGACAACCTGCGCCAAGGATATCCAGAAGGCTGCT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 ValAlaGlyAsnLysAspLeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGlu 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 ATTTACAGAGGAGTT---CGTCTTAGAAAGTCAGGTAAGTGGGTGTGTGAAGTGAGGGAA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 İleTyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArg 419
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                                              GGCATGAACATGGCTTCTCAGGTTGAGGTTAATGACACGACGGATCATGACCTGGACATG 586
                                                                                       AlaGlyGluLeuAlaArgArgLysLysAspAspAspProArgAsnLysAspIleAspTyr 494
                                                                                                                                          GCTGAAGCCGCATTGGCTTTTGAGGCGGAGAAGAGTGATACCACGACGACGAATGATCAT 526
                                                                                                                                                                                                                                                                                                                                AlaTyrAspValAlaAlaIleLysPheArgGlyAlaAsnAlaValThrAsnPhe----- 457
                                                                                                                                                                                                                                                                                                                                                                                                                            CCAAACAAGAAATCTAGGATTTGGCTCGGAACTTTCAAAACAGCTGAGATCGCAGCTCGT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Ver. 2.0
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Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gilmour,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jaglo-Ottosen, Kirsten
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148.50
37.56%
25.85%
4.24%
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                                                                                                                                                                                                                                                                               -----AspīleSerArgTyrAsp 463
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RESULT 13
US-09-198-119C-70
(S-09-198-119C-70)
Sequence 70, Application US/09198119C
Patent No. 6417428
GENERAL INFORMATION:
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Best Local Similarity:
                                                                                                                                   US-10-024-632-2 (1-663) x US-09-198-119C-70 (1-950)
                                                                                                                                                                                                                                                                                                           Alignment Scores:
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SEQ ID NO 70
LENGTH: 950
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-02
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-02
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APPLICANT:
APPLICANT:
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APPLICANT: Jiang, Cai-Zhong
TITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance
FILE REFERENCE: 19117.713 Seq List
CURRENT APPLICATION NUMBER: US/09/198,119C
CURRENT FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 08/706,270
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR APPLICATION NUMBER: US 09/017,816
PRIOR PRIOR DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/017,816
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR APPLICATION NUMBER: US 09/018,235
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Brassica oleracea FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   827 AACCTCTGGAATTAT 841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            520 AspSerGluTrpLysMet-----
420 ValAlaGlyAsnLysAspLeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGlu 439
                                           261 ÁTTTÁCCGÁGGÁGTT---CGCCTTAGAAAATCAGGTAAGTGGGTGTGTGAAGTGAGGGAA 317
                                                                                     400 IleTyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548 AsnCysGlyAsnTyr 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           767 TTACCGCCGCCGTCCGTACAATGGGGACATAATGATGACTTCGAAGGAGATGCTGACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            647 GAGGAGACGACGGTGGAGGGTATTGTTCCGGAGGAACAGATGAGCAAAGGGTTTTACATG 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Ver. 2.0
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Jaglo-Ottosen, Kirsten
Gilmour, Sarah
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1998-02-03
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1998-02-03
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25.36%
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Matches:
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APPLICANT: Zarka, Daniel
APPLICANT: Viang, Cal-Inong
APPLICANT: Viang, Cal-Inong
ITITE OF INVENTION: Blant Having Altered Environmental Stress Tolerance
FILE REFERENCE: 19117.713 Seq List
CURRENT APPLICATION NUMBER: US/09/198,119C
CURRENT FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 09/06,270
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR APPLICATION NUMBER: US 09/017,816
PRIOR APPLICATION NUMBER: US 09/017,816
PRIOR APPLICATION NUMBER: US 09/017,575
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/017,575
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/017,575
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR PRIOR DATE: 1998-02-03
PRIOR PRIOR DATE: 1998-02-03
PRIOR PRIOR PRIOR NUMBER: US 09/018,227
PRIOR FILING DATE: 1998-02-03
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SEQ ID NO 52
LENGTH: 874
TYPE: DNA
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                                                                                                                               PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,234
PRIOR FILING DATE: 1998-02-03
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                                                                                                           NUMBER OF SEQ ID NOS:
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5. 6417428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGAGTGGATGTTCGGGATGCCGACCTTGTTGGCTGATATGGCGGCAGGGATGCTCTTA 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGACGATGGTGGAGGCTGTTTTTACTGAGGAGCAGAGAGACGGGTTTTACATGGCGGAG
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                                                                                 PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TyrAspValGluArgIleMetAlaSerSerAspLeuLeuAla 475
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Gilmour, Sarah
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                                                                                               Sequence 21, Application US/09533029
Patent No. 6664446
GENERAL INFORMATION:
APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Broun, Pierre
APPLICANT: Keddie, James
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
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Best Local Similarity:
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                          APPLICANT:
APPLICANT:
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Samaha, Raymond
Zhang, James
Yu, Guo-Liang
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CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ratcliffe, Oliver
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
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ORGANISM: Arabidopsis thaliana
FEATURE:
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                                                                                                                                                                                                                                                                       AlaTyrAspValAlaAlaIleLysPheArgGlyAlaAsnAlaValThrAsnPheAspIle 459
                                                                                                                                                                                                                                                                                                      ValAlaGlyAsnLysAspLeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGlu 439
                                                                                                                                                                                                                                                                                                                                                                     GTTTATAGAGGGATA---CGTAAGCGTCCATGGGGAAAAATGGGGCGGCTGAGATTCGAGAT
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                       AspSerGluTrpLysMetValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsnGly 539
                                                                                                                                                                                CTGCACCATCCT------CCTCCTCCTAATTATACTCCTCCGCCGTCATCG 522
                                                                                                                                                                                                          SerArgTyrAspValGluArgIleMetAlaSerSerAspLeuLeuAlaGlyGluLeuAla 479
                                                         TGCGTTĠTĊ-----
                                                                                     ThrSerValAsnAsnGluGluThrValGlnValGlnAlaGlyAsnAsnAsnAsnGluAsn 519
                                                                                                                    CCACGATCAACCGATCAGCCTCCGGCGAAGAAG---
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Matches:
Conservative:
Mismatches:
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Gaps:
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 742 CCGAGTCAGCTTGATGAGTCC 762
                          HisAsnMetLeuAspGluSer 581
                                                                                                                                     TTTGGAAATGGGGACGAGTTTCAGAACCTGAGTTACGGATTTGAGCCGGATTATGATCTG
                                                                                                    SerAlaPheSerMetAlaLeuGlnAspLeuIleGlyIleAspSerValGlySerGlyGln 574
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Search completed: March 13, 2004, 08:01:55 Job time: 131 secs

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Run
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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/Ggn2_1/USPTO_Spool/US10024632/runat_09032004_101207_10754/app_query.fasta_1.839
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -QUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10024632 @CGN 1 1 352 @runat 09032004 101207 10754 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN ITIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=120 -YGAPOP=10 -YGAPOR=6 -DELEXT=7
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Listing first 45 summaries
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Perfect score:
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Match
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1: geneseqn1980s:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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Abn84481 Soybean A
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Abn84484 Rice AINT
Aac43005 Arabidops
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Abx13437 A. thalia
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0.510	20007	ACCCOS43	<b>4813</b> 9	d3054	C4670	b3180	k6522	<b>q813</b> 9	C0084	C0079	C0084	C0079	d3034	C0084	c0079	C0079	C0080	C0084	C0079	c0080	d3098	C0084	C0080	0084	c9139	d3 055	c9139	d3033	d3082	d3087	20079	n8448	C0080	0080	C0080	0085
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## ALIGNMENTS

ARRESULT 1
Glycine max Soybean AINTEGUMENTA-like polypeptide GmANT1 cDNA ABN84480; ABN84480 standard; cDNA; 2344 BP He SS, 21-DEC-2000; 2000US-0257896P. 19-DEC-2001; 2001WO-US049294 01-AUG-2002. WO200259332-A2. plant; gene; ss. AINTEGUMENTA; ANT-like polypeptide; GmANT1; soybean; transgenic plant; 21-OCT-2002 (first entry) (MONS ) MONSANTO TECHNOLOGY LLC. Dotson SB Location/Qualifiers 242. .2233 /product= "GmANT1" /*tag=

WPI; 2002-599798/64. P-PSDB; ABB79636.

New nucleic acids encoding AINTEGUMENTA-like polypeptides useful in improving agronomic, horticultural, and quality traits of plants, such increased size of plant organs. 96

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Example 1; Page 127-130; 169pp; English.

The present sequence is that of cDNA encoding GmANT1, a newly identified CC AINTEGUMENTA-like (ANT-like) polypeptide of soybean. The cDNA comprises CC the insert of clone CPR67663, which was obtained from a soybean sequence Cd database screening using Arabidopsis ANT as query. Also isolated was CC clone CPR67626 (see ABN84481) encoding GmANT2 (see ABP9637). GmANT1 and CC GmANT2 show homology to ANT in 2 N-terminal AP2 DNA binding domains, but CC thave C-terminal sequences that bear little, if any, homology to ANT in CC comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding CC comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding CC comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding CC comprising to ANT-like polypeptides have been identified in soybean, CC rice, cotton and corn (see ABB79636-41). Nucleic acids (see ABB480-86) CC encoding the ANT-like polypeptides have been identified in soybean, CC transgenic plants, especially corn, soybean, canola, wheat, cotton, CC tomato or potato (all claimed) having improved agronomic, horticultural CC comprise polyperides (all claimed) having improved agronomic, horticultural CC constoned to the sequence sale technology to CC suppress endogenous ANT-like gene expression, in sense technology to CC modulate expression of endogenous ANT-like gene sthat they are part of, as CC markers for traits linked to those genes, or in the identification of CC loss of function mutant phenotypes of a plant due to a mutation in one or more endogenous genes encoding the ANT-like polypeptides

밁 Ś 문 Ş 밁

Sequence 2344 BP; 738 A; 472 C; 548 G; 586 T; 0 U; 0 Other;

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1682 CGTAAGAAAGATAACGATCCTAGAAACAAGGACATAGACTACAACAAGAGTGTAGTAACA 1741

481 ArgLysLysAspAsnAspPr	461 ArgTyrAspValGluArgII 	441 TyraspValalaalaileLy 	421 AlaGlyAenLysAspLeuTy              1502 GCTGGGAACAAGACCTTTA	401 TyrargGlyValThrargHi 	381 GInGluTyrValAlaHisLe	361 IleAsnPheSerIleGluAs 	341 GluLysalaalaargalaty                1262 GAGAAAGCTGCAAGAGCCTA	321 LysLysGluGlyGlnThrAr             1202 AAGAAGGAAGGCAAACTAG	301 GlyValThrArgHisArgTr              1142 GGTGTCACAAGGCATAGATG	281 LysGlnProValHisArgLy                     1082 AAGCAGCCTGTGCATAGAAA	261 SerGlyThrAspSerValAl	241 LeuGlnSerLeuSerLeuSe 	221 ASNCYSGlyMetGlyASNGl             902 AATTGTGGCATGGGGAATGA	201 AsnTrpValAlaProThrAr	181 LYSGLUThrHisValSerAsp              782 AAGGAAACGCACGTGTCGGAT	161 TYrTYrSerGlyLeuAlaCy:	141 ArgAspLeuLeuSerGlnPro	
oArgAsnLysAspIleAspTyrAsnLysSerValValThr	.eMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArg 	SPheArgGlyAlaAsnAlaValThrAsnPheAspIleSer	TLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAla	SH1BG1nH1BG1yArgTrpG1nAlaArgIleG1yArgVal 	UATGATGLYBSerSerGlyPheSerATGClyAlaSerIle	nTyrGlnValGlnLeuGluGluMetLygAsnMetSerArg                          TACCAAGTTCAACTTGAGGAAATGAAGAACATGAGCAGA	TASPLEUA1AA1ALEULYSTYTTP	glysglyargglnvaltyrleuglyglytyraspmetglu 	pThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCys 	SSEYIleASPThrPheGlyGlnArgThrSerGlnTyrArg	aValaspalalyslysargGlyHisalalysleuGlyGln                         	rMetSerProGlySerGlnSerSerCysValThrAlaPro                         TATGAGTCCTGGTTCTCAGTCTAGTTGTGTCACTGCTCCT	uargasng1yVa1SerLeug1ySerVa1G1yCysG1yG1u 	GGluPheSerThrHisGlnGlnValLeuGluGlnGlnMet 	CysSerSerLeumetFroGlimetThrGluGlyLeuLys                     TGCAGCTCCCTAATGCCTCAAATGACAGAAGGCTTGAAA	SHisGlyLeuTyrGlnAlaProLeuGluGluGluThrThr 1 	OPheArgGlnGlnGlyHisMetSerValGlnThrHisPro 1	
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RESULT 2
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XX ASN
AC ABN8
XX AINT
KW Plan
XX AINT
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XX Glyc
FH Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABN84481;
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New nucleic acids encoding AINTEGUMENTA-like polypeptides useful in improving agronomic, horticultural, and quality traits of plants, such
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)B; ABB79637.
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Query Match: DB:

US-10-024-632-2 (1-663) x ABN84481 (1-2323)

Percent Similarity: Best Local Similarity:

5.51e-134 1715.00 65.86% 54.00% 48.97%

Length:
Matches:
Conservative:
Mismatches:
Indels:

2323 378 83 165 74

Gaps:

Score:

No.:

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                               The present sequence is that of cDNA encoding GmANT2, a newly identified AINTEGUMENTA-like (ANT-like) polypeptide of soybean. The cDNA comprises CC the insert of clone CPR67626, which was obtained from a soybean sequence Cd database screening using Arabidopsis ANT as query. Also isolated was CC clone CPR67663 (see ABN94480) encoding GmANT1 (see ABH96363). GmANT1 and CC GmANT2 show homology to ANT in 2 N-terminal AP2 DNA binding domains, but have C-terminal sequences that bear little, if any, homology to ANT. The CC invention provides nucleic acids encoding ANT-like polypeptides (comprising, in the N-terminal to C-terminal AP2 DNA binding domains, but the CC encoding the ANT-like polypeptides have been identified in soybean, crice, cotton and corn (see ABH9656-41). Nucleic acids (see ABH9480-86) CC encoding the ANT-like polypeptides have been identified in soybean, CC tomato or potato (all claimed) having improved agronomic, horticultural CC or other quality traits, such as increased size of plant organs. These plants are especially useful for production of ethanol or animal federatific acids may also be used in antisense technology to modulate expression of endogenous ANT-like gene expression, in sense co-suppression to makers for traits linked to those genes, or in the identification of compression mutant phenotypes of a plant due to a mutation in one or more endogenous genes encoding the ANT-like polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 134-137; 169pp; English
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Sequence 2323 BP; 746 A; 482 C; 492 G; 603 T; 0 U; 0 Other;

Ś Ś 밁 δ 밁 Ś 밁 밁 S Ś 밁 Ś В δ 439 319 259 199 145 GCTGCTGAAGTGGTTCCTACAAGCTTTTACCACCACACTGCTCCA-----CTTAGTAGC 128 IleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArgAspLeuLeuSerGlnPro 72 53 S <u>α</u> 21 25 92 SerAlaAlaThrValProThrThrPheTyrMetSerProSerGlnSerHisLeuSerAsn ;;;||| MetLysArgIleAsnGluSerAsnAsnThrAspAspGlyAsnAsnHisAsnTrpLeuGly GTTTTTTAC---ATCCAACCCTCACGCCGTGACCCAAATAATAACCAAACCTACCAAAAC CAAGCAATGGCTACTTCAACACCAAAACTGGAGAACTTCTTAGGTGGGGAAGCCATG GlnValMetValProThrSerSerProLysLeuGluAspPheLeuGlyGlyAlaThrMet ATGCCCCTCAAATCTGATGGCTCTCTCTATGGAAACTTTAAGCAGGTCACAAGCA 318 MetProLeuLysSerAspGlySerLeuCysIleLeuGluAlaLeuLysArgSerGlnThr TATGGTTTCTACTATGGACTTGAAGCTGAAAATGTTGGATTGTATTCAGCTTTGCCAATC PheGlyMetCysTyrGlyVal----GlyGluAsnGlyAsnPheHisSerProLeuThrVal TTCTCACTCTCCTCAAATGCATAATATAGGAGTTTCTTCACACTCACAACCTTCCTCT GlyThr---HisGluTyr-----GGGACCCCTCATCACTÁCGAATGTAGTGCCACAGAAACAATGCCTCTGÁGCTTÁGÁCÁGT -GlySerHisGluArgGlyLeuSerLeuAspSer 144 32 84 20 71 52 495 147 127 378 91 258 198 438

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                                                                                                                                                                                                                              <u>AAAGATCTATATCTTGGAACCTTTAGTACACAAGAGGAAGCAGCTGAAGCCTATGATATT</u>
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note= "the CDS does not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetAlaLeuGlnAspLeuIleGlyIleAspSerValGlySerGlyGlnHisAsnMetLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGATGCCGATGCCGGCGCCGGCCGCAGCTCACGTGATGAGGCCGCCGAGTGCCATT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAGCAACTCGAGGGGAGGGCCCTGAGAGGCTTGGCCTCGCCATGCTCTACGCCAAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCCCGGGAGGGAAGATCAGTGGCATCAACTTCTCGAACTCGTCTTCGCTGGTGACTAGC
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                          ANT-like polypeptide;
                                                                                                       /product= "OsANT2"
                                                                                                                                                                location/Qualifiers
                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----CATCCCACCGCCGTCAGCCTCGCCGCCATGAACCCC
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                                                                                                                                                                                                                                                                          OSANT1; rice; transgenic
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Best Local Similarity:
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Pred. No.
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P-PSDB; ABB79639.
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                                                                                                                                                                                         171 GCATGGAGGTGGGCTGTTCTACAACCCTGCCGCCGTCGCCTCCTTC-----TACTA
                                                                                                                                                                                                                                                                            112 GGCGGCGTCGÁCGATGTCGGCCÁCCACCACCÁCCACGTGCACCÁGCAT-CAGCÁGCA
                                             67 rProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeuGluAlaLeuLy 87
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                                                                                                                                                  rGlyValGlyGluAsn----
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1349.50
57.32%
48.02%
38.54%
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                                                                                                                                                                                                                                                                                                                   ThrSerAlaAlaThrValProThrThrPheTyrMetSerProSerGlnSe 48
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Gaps:

-----LeuserAsnPheGlyMetCysTy

170

111 31

----GlyAsnPheHis---Se

67

224 57

284

344

Conservative: Mismatches:

2010 351 68 153 161

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The present sequence is the coding region of the rice OBANT2 gene cancoding a newly identified AINTEGUMENTA-like (ANT-like) polypeptide. The CC enroding a newly identified AINTEGUMENTA-like (ANT-like) polypeptide. The CC OBANT2 gene (see also AEN84483) was isolated following a rice database comparising on the Noterial sequery. Another rice clone (see AEN84482) encoding OBANT1 (see AEN79638) was also collected. The invention provides nucleic acids encoding ANT-like polypeptide sencoding ANT-like polypeptides contained in the Noterial to C-terminal direction, 2 AP2 polypeptides comparising, in the Noterial to C-terminal direction, 2 AP2 polypeptides were identified in those given in AEN79629-35. ANT-like polypeptides were identified in construction of transgenic plants, especially corn, soybean, canola, wheat, cotton, tomato or potato (all claimed) having improved agronomic, comparison, tomato or potato (all claimed) having improved agronomic, comparison, towato or potato (all claimed) having improved agronomic, comparison, towato or potato (all claimed) having improved agronomic, comparison, towato or potato (all claimed) having improved agronomic, comparison, towato or potato (all claimed) having improved agronomic, comparison, towato or potato (all claimed) having improved agronomic, comparison, to suppress endogenous ANT-like gene expression, in sense comparison, to genetically and physically mapping the genes that they are purposes ion to modulate expression of endogenous ANT-like genes, as probes for markers for traits linked to those genes, or in the comparison of endogenous genes encoding the ANT-like due to a construction in one or more endogenous genes encoding the ANT-like due to a construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acids encoding AINTEGUMENTA-like polypeptides improving agronomic, horticultural, and quality traits of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-2001; 2001WO-US049294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 151-154; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            improving agronomic, horticultu
increased size of plant organs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 hrargHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysA 425
                                                                                                                                            385 laHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIleTyrArgGlyValT 405
                                                                                                                                                                                                                                                         365 leGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 alaspala-----LysLysArgGlyHisAla---LysLeuGlyGlnLysGlnProValH 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         695 GCCCCATCATCCCCACCGGCGGCCACCTGCACCCTCTCACCCTGTCCATGAGCTCGGCCG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 ------SerProG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643 -----GGCGGCGGCTACGACATCGCCAACGCCGCCGACGACGTC---TGCGCCCCCG 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 snCysGlyMetGlyAsnGluArgAsnGlyValSerLeuGlySerValGlyCys----- 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 snTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGluGlnGlnMetA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGluGlyLeuLysA 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 -----CAGGGACACGCCCAGGACGGCGGCGCCGTCGGTGGCGACCGCACCACGG 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                            lnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLysLysGluGlyG 325
                                                                                                                CTCACCTCAGAAGGAAAAGCAGTGGCTTCTCGCGTGGCGCTTCGATCTACCGTGGAGTCA 1234
                                                                                                                                                                                                                                                                                                                                               rgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHisIleAsnPheSerI 365
                                                                                                                                                                                                                                                                                                                                                                                                           AGACCAGAAAAGGACGCCAAGTGTATCTTGGTGGGTATGACATGGAGGAGAAAGGCTGCCA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCGCAAGTCCATTGACACGTTCGGCCAGAGGACGTCGCAGTACAGAGGCGTCACCAGGC 934
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                                                                                                                        protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                             Arabidopsis thaliana DNA fragment SEQ ID NO: 37674.
                                                                                                                                                                                                                                              17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                             AAC43005;
                                                 Arabidopsis thaliana
                                                                                             promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                            AAC43005 standard; DNA; 1668 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     635 rpleu---ProSerProThrValGlnMetArgProSerProAla---IleSerLeuSerH 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604 laSerProGluLysArgGlyPro------------SerLeuLeuP 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 leGlyThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerSerArgGluA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 leGly---IleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerSerLysI 584
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Qy 84 GluAlaLeuLyBArgSerGlnThrGlnValMetValProThrSerSerProLyBLeuGlu 103	Qy 64 AsnPheHisSerProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeu 83  Db 232 GGAATCTATTCTCACATGTCTGTGATGCCACTCAGATCTGATGGTTCTCTTTGCTTAATG 291	44 SerProSerGlnSerHisLeuSerAsnPheGlyMetCysTyrG	hrserlaAlaThrValProThrThrPheTyrMet 43     :::::::     CThrThrPheTyrMet 43	21 1 1 0 A	N	tch: 43.2/6 Indels:  Gaps:  Gaps:	Alignment Scores: 1.13e-101 Length: 1668 Pred. No.: 1328.00 Matches: 312 Score: 1328.00 Matches: 69 Percent Similarity: 52.84% Conservative: 69	28-OCT-1999; 99US 28-OCT-1999; 99US 29-OCT-1999; 99US	26-OCT-1999; 99US 26-OCT-1999; 99US 28-OCT-1999; 99US	25-OCT-1999; 99US 25-OCT-1999; 99US 25-OCT-1999; 99US 25-OCT-1999; 99US	PR 21-OCT-1999; 99US-0160814P. PR 21-OCT-1999; 99US-0160815P. PR 22-OCT-1999; 99US-0160980P. PR 22-OCT-1999; 99US-0160981P.	21-OCT-1999; 99US 21-OCT-1999; 99US 21-OCT-1999; 99US 21-OCT-1999; 99US	14-OCT-1999; 99US 14-OCT-1999; 99US 14-OCT-1999; 99US 18-OCT-1999; 99US	13-OCT-1999; 99US 13-OCT-1999; 99US 14-OCT-1999; 99US 14-OCT-1999; 99US	07-0CT-1999; 99US 08-0CT-1999; 99US 12-0CT-1999; 99US 13-0CT-1999; 99US	29-SEP-1999; 99US- 04-OCT-1999; 99US- 05-OCT-1999; 99US- 06-OCT-1999; 99US-	23-SEP-1999; 99US- 24-SEP-1999; 99US- 28-SEP-1999; 99US-
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                                                      ---LeuSerLeuAspSerIleTyrTyrAspSerGlnAsnAlaGluAlaGlnProAspArg
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ATGTTCGGATCAAATATGGGCGGAAATATGAGTCCTTGGACATCAAACCCTAATGCTGAG
                                                                                                                             IleVal ---AsnProIleGlyThrSerValThrSerTrpLeuProSerProThrValGln
                                                                                                                                                        ACTCCCGAGAGACTCTTGAGTTTTCCGGCGATTTTCGCGTTGCCTCAAGTTAATCAAAAG
                                                                                                                                                                                                                                   ThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerSerArgGluAlaSer
                                                                                                                                                                                                                                                                                    GlyIleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerSerLysIleGly
                                                                                                                                                                                                                                                                                                                                                                                           ValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspProArgAsnLysAspIleAspTyrAspLysSerValValThrSerValAsnAspGlu
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                         Thr 663
                                                                           MetArgProSerProAlaIleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp
                                                                                                                                                                                ProGluLysArgGlyProSerLeu-----LeuPheProMetProProMetGluThrLys
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ABX13437 standard; DNA; 2148

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A. thaliana AINTEGUMENTA DNA corresponding to Genbank U40256

RESULT 7
ADX13437
ID ADX13437
AC ABX1
AC ABX1
AC ABX1
AX O4-C
XX O4-C
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DB A. t
DB Expression cassette; transgenic; promoter; LOX5; plant; food production; animal feed; seed; stress resistance; disease resistance; starch content lipid content; dormancy; fibre content; pharmaceutical production; sterile plant; vitamin; flavouring; perfume; dye; cotyledon; embryonic tissue; stress factor; LOX; ds. 11-JUN-2001; 11-JUN-2001; Arabidopsis thaliana 12-DEC-2002. 2001DE-01027882 2001DE-01027882

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-GAGCCCAACACG

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel cassette for the transgenic expression of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis CC thaliana or deletion variants of the LOX5 promoter which are functionally CC linked to the mucleic acid of the invention. The cassette is used to CC prepare transgenic organisms, especially plants, for production of foods, animal feeds, seeds (including those with increased resistance to stress CC and disease, altered starch/lipid contents or dormancy, or altered fibre CC content), pharmacceuticals (especially antibodies, vaccines, enzymes and CC pharmaceutical proteins) and fine chemicals (especially enzymes and CC perfumes and dyes), also to produce sterile plants. The LOX5 promoter CC provides strong and specific expression in cotyledons and/or other early CC embryonic tissue, so can degrade, or protect against, stress factors to CC which these tissues are particularly sensitive. Since cotyledons are the CC cotyledons is homogeneous, there are no side effects on other plant CC organs (pollen) and the promoter is functional value. Expression in the CC cotyledons is homogeneous, there are no side effects on other plant CC entryledons and the promoter is functional value. Expression in the CC cotyledons and the promoter is functional value expression in the CC cotyledons and the promoter is functional value expression in the CC cotyledons and the promoter is functional value expression in the CC cotyledons and the promoter is functional value expression in the CC cotyledons are the promoter is functional value expression in the CC cotyledons are the promoter is functional value. Expression in the CC cotyledons are the promoter is functional value expression and the promoter are no side effects on other plant cotyledons.
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                                                                                                                                                                        GluAlaLeuLysArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGlu 103
                                                                                                                                                                                                                                                                                                                SerProSerGlnSerHisLeuSerAsnPheGlyMetCysTyrGlyValGlyGluAsnGly
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---LeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArg
                                                             GATTICTITGGG-
                                                                                          AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly---
                                                                                                                                       GAAGCTCTCAACAGATCTTCTCACTCGAATCACCATCAAGATTCATCTCCAAAGGTGGAG
                                                                                                                                                                                                                  GGAATCTATTCTCACATGTCTGTGATGCCACTCAGATCTGATGGTTCTCTTTGCTTAATG
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52.84%
43.27%
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                                                             - ACCCATCACAACAACACAAGTCACAAAGAAGCCATG
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                                   IleIysPheArgGlyAlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGlu
                                                                                                      LeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAla
                                                                                                                                                                                           ArgHisHisGlnHisGlyArgTrpGlnAlaArgTleGlyArgValAlaGlyAsnLysAsp 425
                                                                                                                                                                                                                                        CATTTGAGAAGGAAGAGCAGTGGTTTCTCTAGGGGGTGCTTCCATCTATAGAGGAGTCACA
                                                                                                                                                                                                                                                               HisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIleTyrArgGlyValThr
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                                                                                    CTCTACCTTGGAACTTTTGGAACCCAAGAAGAAGCTGCAGAAGCTTACGATGTAGCAGCA
                                                                                                                                                              AGACATCACCAGCATGGAAGGTGGCAAGCACGGATTGGTAGAGTCGCTGGAAACAAAGAT
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                                                                                                                                                                                                                                                          cDNA encoding a Brassica aintegumenta (ANT) polypeptide
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08-JAN-1999;
                         07-JAN-2000;
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reproduction; plant; male sterile plant; female sterile plant
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ATGTTCGGATCAAATATGGGCGGAAATATGAGTCCTTGGACATCAAACCCTAATGCTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating growth and cell proliferation in a plant used to mass, control fertility and enhance asexual reproduction in comprises modulating ANT activity and selecting plants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1738 BP; 500 A; 361 C; 412 G; 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 87; Page 43-44; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fischer RL,
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                                 GAGTTC-
                                                        ProPheArgGlnGlnGlyHisMetSerValGlnThrHisProTyrTyrSerGlyLeuAla
                                                                                   AGTTTATTCTACAATACCACTCATGCG------CCAAACAACAACAACAACTTTCAA
                                                                                                            SerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArgAspLeuLeuSerGln
                                                                                                                                       ---TTTGGGACCCATCATCACAACACAAGTCACAAAGAAGCCATGGATCTTAGCTTAGAT
                                                                                                                                                                                            CATAGTCAAGTT------TCATCTCCAAAGATGGAAGATTTC------
                                                                                                                                                                                                            GlnThrGlnValMetValProThrSerSerProLysLeuGluAspPheLeuGlyGlyAla 109
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Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering phenotypes in plants such as sunflower, coconut, soybean, wheat and
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activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like activity and CKC-like transcription factor activity. Also described: (1) complement (II) of: (I); (2) a chimeric construct (III) comprising (I) or (II); operably linked to a regulatory sequence: (3) a plant (IV) comprising (III) in its genome; (4) seeds (V) obtained from (V); and (5) oil obtained from (V). (I) or its part can be used in antisense inhibition or co-suppression in a transformed plant. (III) is useful for altering the oil phenotype in a plant such as corn, soybean, wheat, rice, canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to ABR40879 represent sequences used in the exemplification of the present invertice.
Sequence 2463
  BP;
  770 A; 539
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521 G; 633 T;
  0 U; 0 Other;
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

7.15e-79 1059.50 47.59% 37.55% 30.25%

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

2463 288 77 202 201 23

Alignment Scores: Pred. No.: Score:

Qy  17 ASTTPLEUGLYPESETLEUSETPTOHISMETLYSMETGIUALATHYSETALALA  197 ANTTTTTAGGTTTTTCCTCTCTCAGAGACACCCTTCTAGAGATCACTCTAA  24 C
17 197 36 257 46 317 485 58 86 106 539 1126 1126 1146
197 197 36 257 46 46 317 74 425 106 106 539 1126 569 1160
197 197 36 257 46 46 317 317 58 86 485 106 539 1126
17 ASNTTPLEUGLYPHESETLEUSETPTOHISMET.  197 AATTTGTTAGGTTTTTCTCTCTCTCAAGAAN  36 ThrValproThrThrPheTyrMetSerPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a comprising a nucleic acid sequence (NS) chosen from a NS encoding a polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIP15-like transcription factor activity and CKC-like transcription factor activity. Also described: (1) cc activity and CKC-like transcription factor activity. Also described: (1) cc complement (II) of (I); (2) a chimeric construct (III) comprising (I) or comprising (III) in its genome; (4) sequence; (3) a plant (IV) and (5) cc comprising (III) in its genome; (4) seeds (V) betained from (IV); and (5) coll obtained from (V). (I) or its part can be used in antisense coll obtained from (V). (I) or its part can be used in antisense constitution or co-suppression in a transformed plant. (III) is useful for canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
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                                                                                                                                               LeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArgAspLeuLeu
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                                                                                                                                                                                                                                                 AACATGAACCAAAACCAACAGCAA--
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                                   IleAspTyrAsnLysSerValValThrSer-------
                                                                                                                                                                 ArgTyrAspValGluArgIleMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArg
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                                                                     CGTTTGÀÀGGATATGGAGCAGGTTGAACTGAGTGTGGÀTÀÀTGGTCATÀGÀGCAGATCAA
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> Cahoon Klein HR. Epelbaum S, Famodu Li C, Oliveira IC, OO, Harvell LT; Sakai H, Shen œ

Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering oil phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.

Claim 18; Page 379-380; 542pp; English.

CC The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (AMP) kinase activity, LIPIS-like transcription factor activity and CKC-like transcription factor activity. Also described: (1) cc complement (II) of (I); (2) a chimeric construct (III) cmprising (I) or CC (II), operably linked to a regulatory sequence; (3) a plant (IV) and (5) cc comprising (III) in its genome; (4) seeds (V) obtained from (IV), and (5) cc inhibition or co-suppression in a transformed plant. (III) is useful for canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to incent construction.

A; 231 Ç 321 <del>ن</del> 324 H •• 0 U; 0 Other;

4.05e-76 1022.00 63.39% 52.63% 29.18% Length:
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Conservative:
Mismatches:
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Υ	243 SerLeuSerLeuSe:	rMetSerProGlySerGlnSerSerCysValThrAlaProSerGly	6
β,	6 AGTTTGTCCCTCAC	AGTTTGTCCCTCACTATGAGCCCCAGTGTGCAAAATGGGGTGGGTGCAATTTCCTCT 62	2
4	263 ThrAspSerValAl	ThrAspSerValAlaValAspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGln	282
Ъ	63 GTTCAAGTGAA		119
٠.	283 ProValHisArgLy	sSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyVal	302
ъ	120 CCAGTTCCTCGCAA	CAGTTCCTCGCAAATCTATTGACACTTTTGGGCAAAAGAACATCTCAATATCGTGGTGTT	179
Α.	303 ThrArgHisArgTr	ThrargHisargTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLys	322
ŭ	180 ACAAGGCATAGATG	GACTGGAAGATATGAGGCCCATTTGTGGGATAATAGTTGCAGAAAG	239
Ÿ	323 GluGlyGlnThrAr	GluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLys 342	342
Ġ.	240 GAAGGGCAAACAAG	GAAAGGAAGGCAAGTTTACCTTGGTGGTTATGATAAGGAAGAAAAA	99
¥	343 AlaAlaArgAlaTy	AlaAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHisIleAsn	362
σ	300 GCAGCAAAGGCTTA	CGACTTAGCTGCACTCAAGTATTGGGGTCCAACAACTCACATAAAT	359
¥	363 PheSerIleGluAsı	PheSerIleGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGlu	382
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LT 13 4483 4483 standard; DNA; 7367 BP. ABN84483; 21-OCT-2002 (first entry) Rice AINTEGUMENTA-like polypeptide OSANT2 gene. AINTEGUMENTA; ANT-like polypeptide; OSANT1; rice; transgenic plant; plant; gene; ds. Oryza sativa.	637 OSETPTOTHTVAIGINMEL	LeusersersrgfluhlaserProglüLysArgGlyProserLeuLeuPheProMet	19AsnAspSerGluTrpLysMetValLeuPheAsnHisProSerGlnGln :::::: 40 TTGTCCAACATGATGTGG	### ### ##############################	### ### ##############################
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the gene encoding OsANT2, a newly identified CC AINTEGUMENTA-like (ANT-like) polypeptide of rice. The gene was isolated CC AINTEGUMENTA-like (ANT-like) polypeptide of rice. The gene was isolated CC following a rice database screening using soybean ANT-like polypeptide CC formall as query. The coding sequence is given in ABN84484. An additional rice clone (see ABN84482) encoding OsANTI (see ABB79638) was also CC isolated. The present invention provides nucleic acids encoding ANT-like CC polypeptides comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding domains followed by an amino acid subsequence selected from CC those given in ABB79629-35. ANT-like polypeptides were identified in CC soybean, rice, cotton and corn (see ABB79636-41). Nucleic acids (see CC ABN84480-86) encoding the ANT-like polypeptides can be used in the CC construction of transgenic plants, especially corn, soybean, canola, wheat, cotton, tomato or potato (all claimed) having improved agronomic, CC wheat, cotton, tomato or potato (all claimed) having improved agronomic, CC wheat, cotton or tomato or potato (all claimed) having improved agronomic, CC construction or enderson potato (all claimed) having improved agronomic, CC animal feedstuff. The nucleic acids may also be used in antisense compression to modulate expression of endogenous ANT-like gene expression, in sense conjugate of genetically and physically mapping the genes that they are probated of agrantic for traits linked to those genes, or in the CC antication in one or more endogenous genes encoding the ANT-like contracted in an or more endogenous genes encoding the ANT-like contracted in the contracted in 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 147-151; 169pp; English.
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                                                                                                                                                          CGGCGGCGGCATGACGCCGTCGTCACCTCCGCGGCCGGCGGCGGATCGTACTATGGCGC
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Qy 633  Db 4893  Qy 651  Db 4953  RESULT 14  ACC00799  ID ACC00799  XX	Db 4650 AC  Qy 563 89  Db 4698 AC  1 Qy 582 er  Db 4739  1 Qy 602 rg  Db 4782 GC  1 Qy 613 eu	Db 4452 AG  Qy 488 rg/  Db 4512 GC0  Qy 508 al0  Db 4545 CC0  Qy 528  Db 4590 CC0  Qy 543 sp	Db 4272 G Qy 433 - Db 4332 T Qy 449 r Db 4392 G Qy 469 1	Qy 432  Db 4092 CTTTTGCGCATGCATGCATGCATGCATGCGGTTGGTTTGGTTTGGCTTTTGTTCGC  Qy 432  Db 4152 TTCCTTTCCAAAGGCTGTGCCCTCGCCGCAGTCGCGTTGGCTTTTTGTTCGCGCGGCGGCGAAAACTC  Qy 432

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                                                                                                                                                                                                                                        The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC polypeptide (PP) having receptor-like protein kinase activity, mitogen CC activity cated protein (MAP) kinase activity, LTP15-like transcription factor CC activity and CKC-like transcription factor activity. SNF1-like CC complement (II) of [I]; (2) a chimeric construct (III) comprising (I) or CC (III), operably linked to a regulatory sequence; (3) a plant (IV) and (5) CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) CC conjustion or co-suppression in a transformed plant. (III) is useful for CC canola, Brassica, sorghum, sunflower or coconsut. (III) is also useful for CC canola, Brassica, sorghum, sunflower or coconsut. (III) is also useful for CC creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00668 and ABR40591 to invention
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                                                                                                                              Percent Similarity:
Best Local Similarity:
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                                                                          US-10-024-632-2 (1-663) x ACC00799 (1-1874)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering oil phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
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Jones TJ,
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P-PSDB; ABR40764.
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                          184 AACTGGCTTTCGTTCTCTCTCCCCA---ATGGAAATGCTCCGAACCTCCGAACCTCAG
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PIONEER HI-BRED INT INC.
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Kinney AJ,
i MC;
 ValProThrThrPheTyrMetSerProSerGlnSerHisLeuSerAsnPheGlyMetCys 56
                                            AsnTrpLeuGlyPheSerLeuSerProHisMetLysMetGluAlaThrSerAlaAlaThr 36
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Klein TM,
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Li C, Oliveira IC, Sakai H, Shen
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  09-AUG-2001; 2001US-0310847P: 19-NOV-2001; 2001US-0336049P:
                                                                                                                                                                                                             Arabidopsis thaliana
                                                                      09-AUG-2002; 2002WO-US025805
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rate; plant vigor; seedling
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g vigor.
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                                                                       The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polynuclectides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
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P-PSDB;
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14-JUN-2002;
Sequence 1818
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DB; ADD30879.
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2002US-00171468.
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Jiang C, Reub
         BP;
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         551 A; 425 C;
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Reuber TL, Creelman RA, Pineda O,
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No. 5.52e-70 951.50 48.61% 36.90% 27.17% Length:
Matches:
Conservative:
Mismatches:
Indels: 1818 252 80 157 194 23

US-10-024-632-2 (1-663) x ADD30878 (1-1818)

Gaps:

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Db dd	62 AATTCTAACAACTGGCTTTGGCTTTTCACCGAACAAC 103	
VΩ	34 AlaAlaThrValProThrThrPheTyrMetSerProSerGlnSerHisLeuSerAsn 52	
Дb	104 TOTTOTTTGCCTCCTCATGAATACAACCTTGGCTTGGTCAGCGACCATATGGACAACCCT 163	
γQ	53PheGlyMetCysTyrGlyValGlyGluAsnGlyAsnPheHisSer 67	
망	164 TTTCAAACACAAGAGTGGAATATGATCAATCCACACGGTGGAGGAGAT 214	
ρy	68 ProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeuGluAlaLeuLys 87	
đb	215 223	
γQ	88 ArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGluAspPheLeuGly 107	
Db	224GAGGTTCCAAAAGTGGCCGATTTTCTCGGT 253	
Ş	108 GlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGlyLeuSerLeuAspSer 127	
Db .	254GTGAGCAAACCGGACGAAAACCAATCCAACCTAGCTAGCT	
γQ	128 IleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArgAspLeuLeuSerGlnPro 147	
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nProlle 628       ::   ACCAGTG 1730	rSerLeuValThrSerLeuSerSerSerArgGluAlaSerProGluLy 608	ArgAsnSerAlaPheSerMetAlaLeuGlnAspLeuIleGlyIleAspSerValGlySer 572	PheAsnHisProSerGln	1229 TACGGTGGTGGCTCGAGCACAGGCTCTGGCTCCACCATCAAGACTTCAAGCTTCAACCT 1288  494 TYFASnLy8SerValValThrSerValAsnAsnGluGluThr 507  495 TACCCTCTAAGCATTCAACAACCATTAGAGCCTTTTCTATCTCTTCAGAACAATGAC 1345  508 ValGlnValGlnAlaGlyAsnAsnAsnAsnGluAsnAspSerGluTrpLy8MetValLeu 527  508 ValGlnValGlnAlaGlyAsnAsnAsnAsnGluAsnAspSerGluTrpLy8MetValLeu 527  11346ATCTCTCATTACAACAACAACAATGCTCACGATTCCTCCTCT 1387

Search completed: March 13, 2004, 05:51:51 Job time : 486 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-MODEL-frame+ p2n.model -DEV=xlh
-Q-/Ggn2 1/USPTO_Spool/US10024632/runat_09032004_101207_10765/app_query.fasta_1.839
-DB=GenEmb1 -QFMT=fastap -SUFFIX=rge -MINMATCH=071_LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pot -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER-US10024632 @CGN 1 1 2860 @runat 09032004 101207 10765 -NCBU-6 -ICPU=3
-NO_MMAP -LARGEOURERY -NEG-SCORES-0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 2000000000
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Ygapop 10.0 , Y
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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461 ArgTyrAspValGluArgIleMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArg 48	TACGATGTAGCGGCGATCAAATTTCGCGGCGCAAATGCAGTCACAAACTTTGACATTTCA	AlaglyAsntysAspLeuTyrLeuGlyThrPhsSerThrGInGluGluAlaAlagluAla 	TyrargGlyVelThrärgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgVal 4		1 IleAsnPheSerIleGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArg	341 GluLysAlaAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHis 360 	21 LysLysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGlu 	301 G1YValThrargHisArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCys 320	281 LysGlnProValHisArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArg 300 	261 SerGlyThrAspSerValAlaValAspAlaLysLysArgGlyHisAlaLysLeuGlyGln 280 	241 LeuGlnSerLeuSerMetSerProGlySerGlnSerSerCysValThrAlaPro 260	221 AsnCysGlyMetGlyAsnGluArgAsnGlyValSerLeuGlySerValGlyCysGlyGlu 240	201 ASnTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGluGlnGlnMet 220 	782 AAGGAAACGCACGTGTCGGATTGCAGCTCCCTAATGCCTCAAATGACAGAAGGCTTGAAA 841		AGAGACCTTCTTCACAACCCTTCAGGGGAACAAGGTCATATGAGTGTCCAAACACCCT	602 AGAGGTTTGAGCCTAGACAGCATCTATTATAACTCCCAAAACGCAGAGGCTCAACCCAAC 661 141 ArgAspLeuLeuSerGlnProPheArgGlnGlnGlvHisMetSerValGlnThrHisPro 160	121 ArgGlyLeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGlnAlaGlnProAsn 140	101 LysLeuGluAspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGlu 1 

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                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 2546)
2 (bases 1 to 2546)
Rieu,I. and Mariani,T.
Direct Submission
Submitted (07-NOV-2003) Plant Control of Noverland Submitted English Plant Control of Noverland Submitted Submitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2546 bp mRNA
Nicotiana tabacum ANT-like protein mRNA,
AY461432
AY461432.1 GI:38492171
                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; eudic
asterids; lamids; Solanales; Solar
1 (bases 1 to 2546)
Rieu, I. and Mariani, T.
A tobacco ANT homolog is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum (common tobacco)
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/culfivar="petit havana SR1"
/db xref=""taxon:4097"
343 2274
note="similar to Arabidopsis thaliana
'codon_start=1
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--AlaAlaThrValProThrThrPheTyrMetSer

CAATATGGAAATCATGAA

798 120 100 690 8 630 62 570 44 510

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960 196 903 REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

FEATURES

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RESULT 2 AY461432 LOCUS

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ECVAIETKKRASGKVVQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCK	זמ
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/protein_id="AAR22388.1"	_

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GGAAATTATAGAAACCCAACTTTTTCCATGGCATTACAAGATCTAATCGGTATTGATTTG
                                      GlyAsnTyrArgAsnSerAlaPheSerMetAlaLeuGlnAspLeuIleGlyIleAspSer 569
                                                                                                                                HisProSerGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLysIleMetAsnCys 549
                                                                                                                                                                           AATGACAACAACAATGGGAATAATGTCACAGATTGGAAAATGGTGTCATAT---
                                                                                                                                                                                                          ValGlnAlaGlyAsnAsnAsnAsnGluAsnAspSerGluTrpLysMetValLeuPheAsn
                                                                                                                                                                                                                                                                                                                                                         SerSerAsnLeuLeuAlaGlyGluLeuAlaArgArgLysLysAspAsnAspProArgAsn 489
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growth and uses thereof
Patent: Wo 02059332-A 3 01-AUG-2002;
Monsanto Technology LLC (US)
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SWEVANFQASHAHESKMIVPHYEENAGESGSIGSMAYCDLQSLSLSMSPSSQSSVTS
SHRASPAVVDSVAMDTKKRGPEKVDQKQIVHRKSIDTFGQRTSQYRGVTRHRWTGRYE
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GTFSTQEEAAEAYDIAAIKFGPANAVTNFDITRYDVEKIMASSNLLSSELARRNRETD
NETQCLDQNHRKFSAYEDTQEAILMHQKSCESENDQWKWVLYGSSQOLLEQNPFTIESD
RTNQSFAVALDNMFHGEYEESKAFTHYSUSPSLATSLSSSREGSPDRTSLPMLSGMP
STASKLLATNPNNVNSWDPSPHLRPALTLPQMPVFAAMTDA"
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/db_xref="taxon:3847"
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	Db 508 CCATTGACGGAAGCAGAGATGCTGCAAGAGGCCGCAGCGCAGCGCCAATGGAAGGCAATGGAAGGCAGCGCAATGGAAGGCAGCAATGGAAGGCAATGGAAGGCAAGAACGCAATGGAAGGAA	153 HisMetSerValGlnThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGln	Qy 113 ThrHisGluTyrGlySerHisGluArgGlyLeuSerLeuAspSerIleTyrTyrAsnSer 132 Db 409 GGCCAT	QY 93 ValMetValProThrSerSerProLysLeuGluAspPheLeuGlyGlyAlaThrMetGly 112

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                                                                                                                                                                                     AK106306.1 GI:32991515
AK106306.1 GI:32991515
PLI_CDNA; oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
         The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satch,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Shishiki,T., Roundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K.,
                                                                                                                                                                                                                                                                                                                                                                                  AK106306
Oryza sativa (japonica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---AspAsnAspProArgAsnLysAspIleAspTyrAsnLysSerValValThrSerVal 502
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Suzuki, Y.,
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A clone:002-101-C10, full
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RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Adachi, J., Pikuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hayatshida, K., Hayatshizaki, Y., Ishida, Y., Ishida, M., Itoh, M., Kada, R., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Inmotani, K., Ratoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kobayashi, M., Kodama, T., Kojima, Y., Knodo, S., Konno, H., Kobayashi, M., Kodama, T., Kojima, Y., Knodo, S., Konno, H., Kobayashi, M., Kodama, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Kusumegi, T., Li, C., Lu, M., Kodama, T., Kodama, T., Miura, M., Miura, J., Miyazaki, A., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, T., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osako, N., Otcomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Sugana, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yongamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                Fals Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Faylimura, T., Kucosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Sugiyama, A., Matsubara, K., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Seiences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken, Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Akimura, T., Arakawa, H., Hiramoto, K., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hara, A., Hashizume, W., Hayashida, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Osato, N., Saikai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibatea, K., Shinagawa, A., Tshirki, T., Sasanishi, A. and Hayashizaki, Y. Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
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Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head (Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (2-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007)
Tel:81-29-838-7007, Fax:81-29-838-7007
This clone is one of the 28K full-length cDNA clones from japoni.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.
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                          sativa (japonica cultivar-group)"
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GinginvalLeugluginginmetAsnCysGlyMetGlyAsnGluArgAsnGlyValSer	617 CAGGGCCA 153 Hismetse 662 CACCAGGT 173 AlaProLe 689 CCATTGAC	Db 494 CCTATCAAGTCCGATGGCTCCCTCTGCATCATGGAAGGC	Db 314 GCTGCTGCTGCTGCCGAAGCCATGTCGTCTCCCCAACAGCCCACAACTTC 373  Qy 42 TyrMetSerProSerGlnSerHisLeuSerAsnPheGly 54	13 GlyAsnAsnHisAsnTrpLeuGly 13 GlyAsnAsnHisAsnTrpLeuGly 14 SecGGCAGCAGCAACTGGTTAGGC 194 GGCGGCAGCAGCAACTGGTTAGGC 33 SerAlaAlaThrValproThrThr 1554 CCGTCCTCCTCGAGCCATCGACT 41	Alignment Scores:  Pred. No.:  1408.50  Score:  Percent Similarity:  55.05*  Best Local Similarity:  46.45*  Mismatches:  152  Query Match:  177  DB:  DB:  DB:  ARIOGROF (1-2510)	/mol_type="mRNA" /cultivat="Nipponbare" /cultivat="Nipponbare" /db_xref="taxon:39947" /clone="002-101-C10"
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935 ATAGGTGGACTGGGAĞATATĞAĞĞCACACCTCTGGĞACAACAĞCĞĞCĞAAĞAAĞĞAĞĞĞC 325 1nThrArgLy8G1yArgG1nValTyrLeuG1yG1yTyrAspMetG1uG1uLysA1aAlaA 	рь Qy рь	S-10-024-632-2 (1-663) x AX555223 (1-2010)  13 GlyAsnAsnHisAsnTrpLeuGlyPheSerLeuSerPro:
	. S &	Percent Similarity: 48.02% Mismatches: 153  Best Local Similarity: 48.02% Mismatches: 153  Query Match: 161  DB: 6 Gaps: 35
u nu (	P & 5	2.48e-82 Length: 1349.50 Matches:
268 alAspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValH	F &	AAASKLYSEVPLNTWASESEAVSSVPARAGVSTAHLEMEAAWTDA"  ORIGIN
251 lySerGlnSerSerCysValThrAlaProSerGlyThrAspSerValAlaV	da Vy	HLRRKSSGESRGASIYRGVTRHHOHGRWOARIGRVSGNEDLYLGTFIASAFAAARRAR HAGTQEEAAEAYDVAAIKFRGLNAVTNFDITRYDVDKILESSTLLPGELARRKGKVGD GGGAAAVADAAALIVQAGNVAEWAATAAALFAAARTEQQQQHGHGGHQHHDLLPSDA FSHI OTHUSTWAA ACA DEDA EHMOMATAAALFAAARTEQQQQHGHGGGGGGU AT ANT BA KE
239GlyGluLeuGlnSerLeuSerLeuSerMetSerProg	g &	GHAQDGGAVGGDPHHGGGGFLQCAVIFGAGAGHDAALVHDQSAAAVAAGWAAMHGGGY DIAMAAADDVCAAGFIFFGGHLEFLTLSWSSAGSQSSCUTVQAAAAGEFYMAMDAVS KKRGAADAAQAQKQPVHRKSIDIFFGQRTSGVRGVTRHRWTGRYEAHLWDNSCKKEEGQTR KGRQNYLGCYNMERKAABAYDLAALKYWGPSTHINFFLEDYORFIFFWKNYMSRQRYVA
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626 GCTGGGCGGCGATGCACATGCAC	? B	D58228.1
01 snTrpValAlaProThrArgGluPheSerThrHisGlnGlnV	§ }	CDS 1
181 ysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGluGlyLeuLysA :::::::: 588 GCTG-GTGGAGACCAGTCCGCCGCGCGGATG	음 성	/db /mo
528 CGGCGGCGGCTCCTGCAGTGCGCTGTCATCCCCGGCGCCCGGCCCACGACGCGGC	₽ \$	Monsanto Technology LLC Location/Qualif
478CAGGGACAGGCCCLAGGACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	g b	Nucleic acid
142 pLeuLeuSerGlnProPheArgGlnGlnGlyHisMet-SerValGlnThrHisProTyrT	γQ	a con a con a
124 rleuaspSerileTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArgAs	Qy Db	SOURCE Oryza sativa ORGANISM Oryza sativa ORGANISM Streptophyta; Embryophyta; Tracheophyta; Sparmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaa; Oryza
105 ELEUGLYGLYALATRIMETGLYTRIHISGLUTYTGLYSETHISGLUARGGLYLEUSE	D QQ	ACCESSION AX555223 VERSION AX555223.1 GI:25898751 KEYWORDS .
	Дb	AX55523 AX55523 2010 bp DNA linear PAT 27-NOV-2002 DEFINITION Sequence 8 from Patent WO02059332.
87 sArgSerGlnThrGlnValMetValProThrSerSerPr	ν,	RESULT 6
67 rProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeuGluAlaLeuLy :::	g 22	Qy 651 LeuSerHisLeuProValPheAlaSerTrpThrAsp 662 :::            :::         Db 2072GCTCATCTCCCTGTTTTTGCAGCCTGGACAGAT 2104
57 rGlyValGlyGluAsn	р Q	Qy 635 TrpLeuProSerProThrValGlnMetArgProSerProAlaIleSer 650
 	₽ 2	1976 CAT
48 rHisLeuSerAsnPheGlvMetCvsTv	Ş	ProProMetGluThrLvsIleValA
32	B &	Oy 598 LeuSerSerSerArgGluAlaSerProGliUysArgGlyProSerLeuLeuPheProMet 617
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The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA; 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida, Satuu,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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/gene="At4g37750"
/codon_start=1
/evidence=experimental
/product="putative ovule
                                                                                                                                                                                                                                                                                        /organism="Arabidopsis
/mol_type="mRNA"
/db_xref="taxon:3702"
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                                                                                                                               /gene="At4g37750"
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/note="This clone i
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Oy  306 ArgTrpThrclyArgTyrGiuAlaHisleuTrpAspknSeyCyslyslygGiuGlyGiu 325  871 AGATGAATAGATGAATGAAGATAGTTTCAAGAAGAAGATACTTCAAGAAGAAGATACTCAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	

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1 (bases 1 to 1965)
Elliott,R.C., Betzner,A.S., Huttner,E., Cakes,M.P., Tucker,W.Q., Gerentes,D., Perez,P. and Smyth,D.R.
AINTEGUMENTA, an APETALA2-like gene of Arabidopsis with pleiotropic roles in ovule development and floral organ growth
Plant Cell 8 (2), 155-168 (1996)
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Arabidopsis thaliana ANT (AINTEGUMENTA) mRNA,
U41339
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Monash University, Wellington Road, Clayton, V
Location/Qualifiers
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                                                                /gene="AINTEGUMENTA"
/note="similar to APETALA2 protein
Accession Number U12546"
                                                                                                                                       /map="between spt and
/tissue_type="flower;
. . 1905
                                                                                                                        gene="AINTEGUMENTA"
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'db_xref="taxon:3702"
                                                                                                                                                                                                                                    organism="Arabidopsis thaliana"
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|||
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/note="ecodes second
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SSHSNHHQDSSPKVEDPFGTHHINNTSHEAMDLSLDSLFYNTTHEBNTTNFGBFFSF
PQTRNHEEETRNYGNDPSLTHGGSFNVGVVGEFQQLSLSSLSVBGSGSGSCTGGSHHQQ
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AALKYMGPSTHTNFSAENYQKEIEDMKNMTRGEVYAHLRRKGSFSRKASIYBOVTH
HQHGRWQARIGRVAGNKDLYLCTFGTQEEAABAYDVAAIKFRGTNAVTNFDITRYDVD
RIMSSNTLLSGELARBNNNSIVVRNTEDQTALNAVVBGGSNKEVSTPRRLLSFPAIFA LPQVNQKMFGSNMGGNMSPWTSNPNAELKTVALTLPQMPVFAAWADS"

SerProSerGlnSerHisLeuSerAsnPheGlyMetCysTyrGlyValGlyGluAsnGly TCATCTTCAACTTCTCAGCTGCAACTTCTTCTTCTTCTGTTCCACCTCAACTTGTTGTT AsnPheHisSerProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeu ----GACAACACTAGCAACTTTGGTGTTTTGCTATGGATCTAACCCAAATGGA 83 268 63

GGAATCTATTCTCACATGTCTGTGATGCCACTCAGATCTGATGGTTCTCTTTGCTTAATG 103 328

GluAlaLeuLysArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGlu

388

AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly---

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ThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuGluGlu 177 AspLeuLeuSerGlnProPhe------ArgGlnGlnGlyHisMetSerValGln 157 ACTACAAACTTTCAAGAGTTCTTTAGCTTCCCTCAAACCAGAAACCAT-GAGGAA 541 535

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566 GlyIleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerSerLysIleGly 1527	Qy         506         GluThrValGlnValGlnAlaGlyAsnAsnAsnGluAsnAspSerGluTrpLysMet         525           Db         1504         GAA	QY  446 ATTAAGTTCCGTGGCACAAATGCTGTGACTAACTTTGATATCACGAGGTACGATGTTGAT  QY  466 ATGILEMETALGSESERASHLEULEUALAGTGAGGTACGAAGGTACGATGTTGAT  QY  466 AGGILEMETALGSESERASHLEULEUALAGTGGTGGCGAAGGTACGATGTTGAT  1425  Db  1426 CGTATCATGTCTAGTAACACACTCTTGTCTGGAGAGGTAGCGAAGGAACC  1476  QY  486 ASPPTOATGAGTAACACACTCTTGTCTGGAGAGGTATGTCC	366 HISLENARGLYSES ELSEIGLY PRESERRIGUS YALASELLES YEARGELY VILLE III	1006 AGTAGAAAAGGACAAGATTTATCTGGGAGGTCCCTCTACTAGAGAAGACTGCTCGGAGGAGAAAAGCTGCTCGAGAGAAAAGGAAGAAGATTTATCTGGGAGGAGAAAAGCTGCTCGAGAGAAAAGCTGCTCGAGAGAAAAGCTGCTCGAGAGAAAAGCTGCTCGAGAGAAAAGCTGCTCGAGAGAAAAGCTGCTCGAGAGAAAAGCTGCTCGAGAATTTCTCTGCGGAGGAGACACAACAATTTCTCTGCGGAGAGACAGAC	3 8 8 8 6 3 9 4 6 6 6 8 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8

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Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Garninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Street, Albany, CA 94710, USA
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.I., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinn, P., Sakurai, K., Davis, R.W., Ecker, J.R. and Theologis, A.
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                                                                                                                                                                                                                                                                   Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Banh, J., Chan, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Chodera, C.S., Quach, H.L., Tang, C.C., Goldsmith, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                         genome
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                                                                                                                                                                                         Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 2056)
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  (R11873)"
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US-10-024-632-2 (1-663) x AY080706 (1-2056)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 TCATCTTCAACTTCTTCAGCTGCAACTTCTTCTTCTTCTGTTCCACCTCAACTTGTTGTT
                                                                                                                                                                                                                                                                                                                                                                          64 AsnPheHisSerProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeu
GATCTTAGCTTAGATATTTATTCTACAACACCACTCAT-----GAGCCCAACACG
                                                                                                                                                                                                                                                                                                                                      GGAATCTATTCTCACATGTCTGTGATGCCACTCAGATCTGATGGTTCTCTTTGCTTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerProSerGlnSerHisLeuSerAsnPheGlyMetCysTyrGlyValGlyGluAsnGly
                                                      ---LeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArg 141
                                                                                                                                                                                                                            GAAGCTCTCAACAGATCTTCTCACTCGAATCACCATCAAGATTCATCTCCAAAGGTGGAG
                                                                                                                                                                                                                                                                            GluAlaLeuLysArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGlu
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                                                                                                                                                                   AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTCATTGTCTTCAAATATGATGAAAATGGGAGGTAGAGGAGGTAGAGAAGCTATTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative ovule development protein aintegumenta"
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RIMSSNTILSGELARRANNSITVRNNTEDQTFALMAVVEGGSURGVSTPERLLSFPAIFA
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(Lambda ZAP) as a XhoI/SstI insert."
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52.84%
43.27%
37.92%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GluAlaThrSerAlaAlaThrValProThrThrPheTyrMet 43
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                                                                                                                  - ACCCATCACAACAACACAGTCACAAAGAAGCCATG
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유 뫄 8 멍 5 밁 S

| STRGCA 1267  ValThr 405                                     STCACA 1327  STCACA 1327  ADADGAT 1387   TTAACTTC                                                                |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|
|                                                                                                                                                                                                                                                                                                                                                  | 446 IleI                                                                |
| 4444                                                                                                                                                                                                                                                                                                                                             | 426 LeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAla<br>    |
| 4 4                                                                                                                                                                                                                                                                                                                                              | 406 ArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysAs<br>     |
| ш                                                                                                                                                                                                                                                                                                                                                | 386 HisleuargarglysserSerGlyPheSerargGlyAlaSerIleTyrArgGlyValThr<br>    |
| ValAla 385                                                                                                                                                                                                                                                                                                                                       | 366 GluasnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValAla<br>    |
| Serile 365<br>   <br> CTGCG 1207                                                                                                                                                                                                                                                                                                                 | 346 AlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHisIleAsnPheSerIle<br>    |
| AlaArg 345<br>      <br> STCGA 1147                                                                                                                                                                                                                                                                                                              | 326 ThrarglysglyargglnValTyrLeuglyGlyTyrAspMetGluGluLysalaalaar: .::    |
| 31yGln 325<br>   <br>3GTCAC 1087                                                                                                                                                                                                                                                                                                                 | 306 ArgTrpThrGlyArgTyrGluAlaHiBLeuTrpAspAsnSerCysLyBLySGluGlyGln<br>    |
| ArgHis 305<br>      <br>AGACAT 1027                                                                                                                                                                                                                                                                                                              | 286 ArglysSerileAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHis<br>    |
| ValHis 285                                                                                                                                                                                                                                                                                                                                       | 269 AspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHis                 |
| Alaval 268<br>   <br>3CGGCT 907                                                                                                                                                                                                                                                                                                                  | 262GlyThrAspSerValAlaVal                                                |
| CACCAG 847                                                                                                                                                                                                                                                                                                                                       | 258 ThrAlaProSer                                                        |
| 7 2                                                                                                                                                                                                                                                                                                                                              | 38 CysGlyGluLeuGl<br>  <br>40CA                                         |
| ValGly 237                                                                                                                                                                                                                                                                                                                                       | 218 GlnGlnMetAsnCysGlyMetGlyAsnGluArgAsnGlyValSerLeuGlySerV             |
| LeuGlu 217                                                                                                                                                                                                                                                                                                                                       | -; ;;                                                                   |
| ChrGlu 197                                                                                                                                                                                                                                                                                                                                       | 178 GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetDroGlnMetThrGlu        |
| JG1UG1U 177<br>      <br> -GAGGAA 661                                                                                                                                                                                                                                                                                                            | 158 ThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuG<br> <br>656 |
| /alGln 157                                                                                                                                                                                                                                                                                                                                       | 142 AspleuLeuSerGlnProPheArgGlnGlnGlyHisMetSerVa                        |

	TCT 1822	1820	뮍
	Thr 663	663	8
1819	CTTAAGACCGTCGCTCTTACTTTGCCTCAGATGCCGGTTTTTCGCTGCTTGGGCTGAT	1763	망
662	MetArgProSerProAlaIleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp	643	ĮQ.
1762	ATGTTCGGATCAAATATGGGCGGAAATATGAGTCCTTGGACATCAAACCCTAATGCTGAG	1703	Δp
642		624	γŞ
1702	ACTCCCGAGAGACTCTTGAGTTTTCCGGCGATTTTCGCGTTGCCTCAAGTTAATCAAAAG	1643	В
623	ProGluLysArgGlyProSerLeuLeuPheProMetProProMetGluThrLys	606	γQ
1642		1610	B
605	ThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerSerArgGluAlaSer	586	Qy
1609		1609	g U
585	GlyIleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerSerLysIleGly	566	Qy
1609	GCTCTAPATGCT	1598	<b>g</b>
565	<pre>IleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSerMetAlaLeuGlnAspLeuIle</pre>	546	83
1597	GACCAAACC	1589	рb
545	ValLeuPheAsnHisProSerGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLys	526	Ş
1588	GAA	1586	뫄
525	GluThrValGlnValGlnAlaGlyAsnAsnAsnAsnGluAsnAspSerGluTrpLysMet	506	VQ V
1585	AACAACAGCATTGTCGTCAGGAATACT	1559	뫄
505	AspProArgAsnLysAspIleAspTyrAsnLysSerValValThrSerValAsnAsnGlu	486	γQ
1558		1508	gg

REFERENCE AUTHORS TITLE JOURNAL

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 11 BD274516 LOCUS DEFINITION

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COMMENT

773 198 812 218 815	ArgGlnGlnGlyHisMetSe ::: CCCTCAAACCAGAAACCAT sHisGlyLeuTyrGlnAlaProLe	Db 560 GAAGCTCTCAACAGATCTTCTCACTCGAATCACCATCAAGATTCATCTCCAAAGGTGGAG 619  Qy	449 GGTGACAACACTAGCAACTTTGGTGTTTGCTATGGATCTAACCCAAATGGA 49 64 AsnPheHisSerProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeu 83 65 GAATCTATCTCACAATGTCTGTGATGCCACTCAGATCTAATGGTTTTGCTTAATG 66 GAATCTATTCTCACAATGTCTGTGATGCCACTCAGATCTGATGGTTTTTTTT	Qy 21 PheSerLeuSerProHisMetLysMet 29             :::	US-10-024-632-2 (1-663) x BD274516 (1-2148)  Qy	Alignment Scores: 7.84e-81 Length: 2148  Pred. No.: 1328.00 Matches: 312  Percent Similarity: 52.84* Conservative: 69  Best Local Similarity: 43.27* Mismatches: 116  Query Match: 37.92* Indets: 224  DB: 6 Gaps: 21	FH Key Location/Qualifiers FT CDS (269)(1936) FT misc_feature (1109)(1339) FT misc_feature (1340)(1414) FT misc_feature (1415)(1621). FEATURES Location/Qualifiers Source 12148 //organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702"
Qy 526 ValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGinLys 545  Db 1700	1619 CGTARCATGTCTAGTAACACACTCTTGTCTGGAGAGTTAGCGGGAAGGAA	QY 426 LeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAla 445	Db 1319 ĠAĠAĀTĀTCĀĠAAAGĀGĀTTĠAĀGĀCĀTĠAĀGĀĀCĀĀĠĀĀĀĀĀĀTĀTĠCĀ 1378  Qy 386 HiBLewĀrgĀrgVpSSerSerGlyPheSerArgGlyAlaSerIlefYrĀrgGlyValfhr 405	Db 1199 AGTAGAAAAGGAAGACAAGTTTATCTGGGAAGTTATGATATGAAGGAGAAAAGCTGCTCGA 1258  Qy 346 AlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHisIleAsnPheSerIle 365  Qy 1259 GCATATGATCTTGCTGCACTCAAGTACTGGGGTCCCTCTACTCACCAATTTCTCTGGG 1318  Db 1259 GCATATGATCTTGCTGCACTCAAGTACTGGGGTCCCTCTACTCAACCAATTTCTCTGGG 1318  Qy 366 GluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValAla 385	306 ATTTPTTTTCIALCATACTILIUGAACTCATUCATACTCATACATACTCATACATACTCATACATA	959 CAGATCTCTGAAGCTCTTGTGGAGACAAGCGTTGGGTTTGAGACGACGACAATGGCGGCT 269 AspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGinProValHis 1019 GCGAAGAAGAAGAGAGACAAGAGATTGTTGTAGTTGATCAGAAACAGATTGTTCAT 286 ArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHis 11	38 CysGlyGluLeuGlnSerLeuSerLeuSerMetSerProGlySerGlnSerSerCysVal

1 MetLysArgileAsnGluSer               269 ATGAAGTCTTTTTGTGATAAT 21 PheSerLeuSerProHis	/mol_type="genomic DNA"  Alignment Scores: 7.84e-81 Length: 2148 Pred. No.: 1328.00 Matches: 312 Score: 1328.00 Matches: 59 Percent Similarity: 52.84* Conservative: 69 Best Local Similarity: 43.27* Mismatches: 116 Query Match: 37.92* Indels: 224 DB: 663) x AR316367 (1-2148)	Unknown. Unknown. Unclassified. 1 (bases 1 to 2148) Fischer, R. L. and Mizukami, Y. Methods for altering mass ar Patent: US 6559357-A 1 06-M2 Location/Qualifiers 1. 2148 /organism="unknown"	Qy 663 Thr 663 :: Db 1931 TCT 1933  RESULT 12 AR316367 LOCUS AR316367 DEFINITION Sequence 1 from patent US 6559357. ACCESSION AR316367 ACCESSION AR316367 GI.31711158	Db 1754 ACTCCCGAGÁGACTCTTGÁGTTTTCCGGCGATTTTCGCGTTGCÓTCAAGTTAATCAAÁÁG 1813  Qy 624 IleValAsnProlleGlyThrSerValThrSerTrpLeuProSerProThrValGln 642 ::::::::::::::::::::::::::::::::::::	Qy       566 GlyIleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerSerLysIleGly 585         Db       1720 1720         Qy       586 ThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerSerArgGluAlaser 605         Db       1721
B	D Q D Q	5 B B B B B B	00 AG AG AG	P Q B Q B	소 용 호 용 호
306 ArgitpinfolyArgiyrciuAlaHisLeutrpAspAsnserCysLysLySGliGLYGLI 325 1139 AGATGGACTGGTAGATATGAAGCTCATCTATGGGACAATAGTTTCAAGAAGGAAG	62	GGGTCTTTTAATGTAGGGGTATATGGGGGAATTTCAA	178 GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu 197	668 GATCTTAGCTTAGATAGTTTATTCTACAACACCACTCATGAGGACCACACAC 718  142 AspLeuLeuSerGlnProPhe	84 GluAlaLeuLysArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGlu 103 560 GAAGCTCTCAACAGATCTCTCACTCGAATCACCATCAAGATTCATCTCCAAAGGTGGAG 619 104 AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly 122

RESULT 13 AR427901 AR427901 AR427901 AR427901  DEFINITION Sequence 1 from patent US 6639128.  ACCESSION AR427901 AR427901  ORBSION AR427901  INCRES Unknown. ORGANISM Unclassified. REFERENCE AUTHORS FISCHER, L. and Mizukami, Y. FITTLE Enhancing asexual reproduction in plants FEATURES FOURCE JOURNAL FATERICE Fatent: US 6639128-A 1 28-OCT-2003; FEATURES SOURCE  JOURNAL FEATURES Location/Qualifiers	Qy 663 Thr 663 Db 1931 TCT 1933	ATGTTCGGATCAATATGGCCGAAATATAGGTCCTTGGACATCAAACCCTAATGCTGAG MetArgProSerProAlaileSerLeuSerHisLeuProValPheAlaSerTrpThrAsp :::::: :::::::::::::::::::::::::::::	172 60 60	Db 1700	Qy       466 ArgIleMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArgArgLysLysAspAsn 485         Db       1619 CGTATCATGTCTAGTAACACACTCTTGTCTGGAAGAGTTAGCGCGAAGGAAC 1669         Qy       486 AspProArgAsnLysAspIleAspTyrAsnLysSerValValThrSerValAsnAsnGlu 505         Db       1670	Qy 406 ArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysAsp 425
Db       773 ĠĂÁČĆTAGAAATTACGGGAATGÁČ		142 AspleuLeuSerGlnProPheArgGlnGlnGlyHisMetSerValGln	Db 560 GAAGCTCTCAACAGATCTCTCACTCGAATCACCATCAAGATTCATCCTCCAAAGGTGGAG 619  Qy 104 AspPheLeuGlyGlyAlaThrWetGlyThrHisGluTyrGlySerHisGluArgGly 122	Oy  44 SerProSerGlnSerHisLeuSerAsnFheGlyMetCysTyrGlyValGlyGluAsnGly 63  11	US-10-024-632-2 (1-663) x AR427901 (1-2148)  QY  1 MetLysArgIleAsnGluSerAsnAsnThrAspAspGlyAsnAsnHisAsnTrpLeuGly 20	/organism="unknown"  ORIGIN  Alignment Scores: 7.84e-81 Length: 2148 Score: 7.84e-81 Matches: 312 Percent Similarity: 52.84* Conservative: 69 Best Local Similarity: 43.27\$ Mismatches: 116 Query Match: 6 Gaps: 21

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                                                                             ThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerSerArgGluAlaSer 605
                                                                                                                                                                                        GlyIleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerSerLysIleGly
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                            ----GTTGTGGAAGGTGGTTCCAACAAGAAGTCAGT 1753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (07-NOV-1995) L. Reiser, Plant Biology,
Koshland Hall, Berkeley, CA 94720, USA
Location/Qualifiers
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1 (bases 1 to 2148)

Klucher, K.J., Chow, H., Reiser, L. and Fischer, R.L.

Klucher, K.J., Chow, H., Reiser, L. and Fischer, R.L.

Gametophyte Development is Related to the Floral Homeotic Gene
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y 518 GluAsnAspSerGluTrpLysMetValLeuPheAsnHisProSerGlnGlnGlnGlnAla b 1459 GTG	AsnGlyAsnG   G		1488	578 LeuAspGluSerSerLysIleGlyThrHisPheSerAsnThrSerSerLeuValThrSer	1488	598 LeuSerSerArgGluAlaSerProGluLysArgGlyProSerLeuLeuPheProMet	1489CCGACGATATTTG		ProProMetGluThrLysIleValAsnE		
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Search completed: March 13, 2004, 07:10:13 Job time : 4737 secs

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equence 1,	US-10-059-911-1		.~	132
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## ALIGNMENTS

RESULT 1 US-10-024-632-1

Sequence 1, Application US/10024632 Publication No. US20020170093A1

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GENERAL INFORMATION:
APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
APPLICANT: Dotson, Stanton B.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION
TITLE OF INVENTION: UNCLEER: US/10/024,632
CURRENT FILLING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR FILLING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEO ID NO
LENGTH: 2344
TYPE: DNA
ORGANISM: Glycine max
PEATURE:
NAME/KEY: CDS
LOCATION: (242)..(2233)
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21 PRESENTENSE PROFISHE LINGUISTAND AND THE SERVING THE ACTUAL OF THE ACTUAL CONCECNION AND THE ACTUAL CONCECNION AND THE ACTUAL CONCECNION AND THE ACTUAL CONCECNION AND THE ACTUAL CONCECNION AND THE ACTUAL CONCECNION AND THE ACTUAL CONCECNION AND THE ACTUAL CONCECNION AND THE ACTUAL CONCECNION AND THE ACTUAL CONCECNION AND THE ACTUAL CONCECNION AND THE ACTUAL CONCENTRATION AND THE ACTUAL C	; OTHER INFORMATION: US-10-024-632-1  Alignment Scores: Pred. No.: Score: 100.00\$ Percent Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Best Local Sim
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Pred. No.:
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APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 136491
LENGTH: 2405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Glycine max
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GluGluGluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMet 195
                                                                                                                                                                        GluAlaGlnProAsnArgAspLeuLeuSerGlnProPheArgGlnGlnGlyHisMetSer 155
                                                                                     ValGlnThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeu 175
                                                                                                                                                                                                                                                          TyrGlySerHieGluArgGlyLeuSerLeuAepSerIleTyrTyrAenSerGlnAenAla 135
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                                                GTCGAAACACACCCTTATTACTCTGTATTTGCTTGTCGAGGTTTTGTATCAGGCACCGTCG 1338
                                                                                                                                        GAGGCTCAACCCAACAGAAACCTTCTTTCACATCCCTTCAGGCAACAAGGGCATGTGAAT 1278
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                                                                                                      454 ValThrAsnPheAspIleSerArgTyrAspValGluArgIleMetAlaSerSerAsn 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 LeuTrpAspAsnSerCysLysLysGluGlyGlnThrArgLysGlyArgGlnValTyrLeu
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                                                                                                                                                           CAAGAGGAAGCAGAAGCATACGATGTAGCGGCGATCAAATTTCGCGGCGCAAATGCA 2346
                                                                                                                                                                                                     GlnGluGluAlaAlaGluAlaTyrAspValAlaAlaIleLysPheArgGlyAlaAsnAla 453
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                                                                      GTCACAAACTTTGACATTTCAAGATACGATGTGGAGAGAATCATGGCCAGTAGCAAT
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Sequence 18711, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
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CONTROL TORON Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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TITLE OF INVENTION:
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Best Local Similarity:
Query Match:
DB:
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; OTHER INFORMATION: Clone ID: LIB3109-011-F8_FLI
US-10-425-114-18711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                         176 GluGluGluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMet 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheSerLeuSerProHisMetLysMetGluAlaThrSerAlaAlaThr------ 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrGlySerHisGluArgGlyLeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAla 135
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   GAGGAAGAAGCAACAAAGGAAACGCACGTT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProThrSerSerProLysLeuGluAspPheLeuGlyGlyAlaThrMetGlyThrHisGlu 115
                                                                                                                          GTCGAAACACACCCTTATTACTCTGTATTTGCTTGTCGAGGTTTGTATCAGGCACCGTCG 816
                                                                                                                                                                                ValGlnThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeu 175
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Conservative:
Mismatches:
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                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                              ; LOCATION: (25)..(2; OTHER INFORMATION: US-10-024-632-3
US-10-024-632-2 (1-663) x US-10-024-632-3 (1-2323)
                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWALL,
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10024632

Publication No. US20020170093A1

GENERAL INFORMATION:

APPLICANT: MORBANTO Technology LLC

APPLICANT: He, Steve S.

APPLICANT: DOCSON, STANION B.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION

TITLE OF INVENTION: GROWTH AND USES THEREOF

FILE REFERENCE: 38-21(51837)B USES THEREOF

FILE REFERENCE: 38-21(51837)B USES THEREOF

CURRENT APPLICATION NUMBER: US/10/024,632

CURRENT APPLICATION NUMBER: US/10/024,632

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: US 60/257,896

PRIOR FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 33

NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Indels:
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ercent Similarity: 55.05% est Local Similarity: 46.45% uery Match: 13  S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x US-10-024-63; S-10-024-632-2 (1-663) x	CCANT: He, Steve S.  CCANT: Dotson, Stanton B.  OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIAT  OF INVENTION: GROWTH AND USES THEREOF  REFERENCE: 38-21(51837)B  ENT APPLICATION NUMBER: US/10/024,632  SMT FILING DATE: 2001-12-19  R APPLICATION UNMBER: US 60/257,896  R FILING DATE: 2000-12-21  R OF SEQ ID NOS: 33  WARE: Patentin version 3.1  D NO 5  STH: 1926  B: DNA  ANISM: Oryza sativa  TURE:  ENTORNATION:  (1)(1926)  ENTORNATION:  24-632-5  1408.50  Matches:  1408.50  Matches:  1408.50  Matches:  1108.50  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Matches:  Mat
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US-10-024-632-2 (1-663) x US-10-024-632-8 (1-2010)  Qy	t Similarity: 57.32% ocal Similarity: 48.02% Match: 13	S Length:	LOCATION: OTHER INFO S-10-024-632-		SOFTWARE: SEQ ID NO LENGTH:	CURRENT FILING DATE: 2001-12-19 FRIOR APPLICATION NUMBER: US 60/257,896 FRIOR FILING DATE: 2000-12-21 FRIOR FILING DATE: 2000-12-21	APPLICANT: DOCEON, STANTON B. TITLE OF INVENTION: NUCLEIC ACID MOLEC TITLE OF INVENTION: GROWTH AND USES T FILE REFERENCE: 38-21 (51837) B	Publication GENERAL INFO APPLICANT: APPLICANT:	RESULT 6 US-10-024-632-8 ; Sequence 8, Application US/10024632	Qy 651 LeuSerHisLeuProValPheAlaSerTrpThrAsp 662 :::             :::         Db 1891GCTCATCTTCCCTGTTTTTGCAGCCTGGACAGAT 1923	QY 635 TrpLeuProSerProThrValGlnMetArgProSerProAlaileSer 650	Qy 618 ProProMetGluThrLysIleValAsnProIleGlyThrSerValThrSer 634 bb 1795 CAT	Qy 598 LeuSerSerArgGluAlaSerProGluLysArgGlyProSerLeuLeuPheProMet 617	QY 579 AspGluserSerLysIleGlyThrHisPheSerAsnThrSerSerLeuValThrSer 597	Qy 559 MetAlaLeuGlnAspLeuIleGlyIleAspSerValGlySerGlyGlnHisAsnMetLeu 578	Qy 539 GlyAsnGlySerAspGlnLysIleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSer 558	Qy 523 TrpLysMetValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsn 538	
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325 lnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaA 345 	875 ACCGCAAGTCCATTGACACGTTCGGCCAGAGGACGTCGCAGGACGACGAGGACGAGTACAGGCGTCACAGGCGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	isArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgH	268 alaspalaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnDroValH 285	251 lySerGlnSerSerCysValThrAlaProSerGlyThrAspSerValAlaV 268	239GlyGluLeuGlnSerLeuSerMetSerProd 251		201 snTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGluGlnGlnMetA 221						87 sArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGluAspPh 105 :::	67 rProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeuCluAlaLeuLy 87 : ::		7-7		

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1415 TCAACGCCGTCACCAACTTCGACATCACGAGGTACGACGTGGACAAGATCCTGGAGAGAGCA 1474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 leGly---IleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerSerLysI 584
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                         ACCTGCCAATGTTCGCCGCGTGGACCGAC 2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CACCATGACCTCCTGCCGAGCGACGCCTTCTCGGTG---CTGCAGGACATCG 1720
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                                                                                                                               GGGCCTCGCCTCGCCGGCGGTGAGCTCGGTGCCGGCGAGGGCCGGCGTGTCCATCGCGC 1975
                                                                            isLeuProValPheAlaSerTrpThrAsp 662
                                                                                                                                                                               rpLeu---ProserProThrValGlnMetArgProSerProAla---IleSerLeuSerH 653
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APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass in Plants
FILE REFERENCE: 023070-090730US
CUURRENT APPLICATION UNMER: US/10/059,911
CURRENT PILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2148
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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LOCATION: (269)..(1936)
COTHER INFORMATION: Arabidopsis AINTEGUMENTA (ANT)
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158 ThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuGluGlu 177
                                                                                                                                                                                                                                                                                                           104 AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly---
                                                                                                                                                        668 GATCTTAGCTTAGATAGTTTATTCTACAACACCACTCAT-----GAGCCCAACACG 718
                                                                                                                                                                                                        123 ---LeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArg 141
                                                                                                                                                                                                                                                                                                                                                                    560 GAAGCTCTCAACAGATCTTCTCACTCGAATCACCATCAAGATTCATCTCCAAAAGGTGGAG
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                                                     ACTACAAACTTTCAAGAGTTCTTTAGCTTCCCTCAAACCAGAAACCAT-------
                                                                                                  AspLeuLeuSerGlnProPhe-----ArgGlnGlnGlyHisMetSerValGln 157
                                                                                                                                                                                                                                                                                                                                                                                                                 GluAlaLeuLysArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGlu 103
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	486 AspProArgAsnLysAspIleAspTyrAsnLysSerValValThrSerValAsnAsnGlu 505
	466 ArgileMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArgArgLysLysAspAsn 485
	446 IleLysPheArgGlyAlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGlu 465 
	426 LeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAla 445 
	406 ArgHisHisGlnHisGlyArgTrpGlnAlaArgTleGlyArgValAlaGlyAsnLysAsp 425 
	386 HisleuargargLysSerSerGlyPhcSerargGlyAlaSerIleTyrargGlyValThr 405 
	366 GluaenTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValAla 385 
	346 AlaTyraspleualaalalaleulysTyrTrpGlyProSerThrHisIleAsnPheSerIle 365 
· · · · · ·	326 ThrarglybglyargglnValTyrLeuglyglyTyrAspMetGluGluLysAlaAlaArg 345 
	306 ArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLysGluGlyGln 325
	286 ArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHis 305 
	269 ABPALALYSLYSATGGIYH15AlaLySLeuGlyGlnLySGlnDroValHis 285
	262GlyThrAspSerValAlaVal 268
	258 ThrAlaProSer 261
	SerLeuSerMetSerProGlySerGlnSerSerCysVal 25 
<del></del> -	GlySerValGly 23
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	286 ArglysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHi	691 CAGATCICTGAAGCTCITGIGGAGACAAAGGACGACGGC 761 AspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHis 761 AspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHis 761 AspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHis 7761 AGGAAGAAGAAGAGAGAGAAGAAGAAGAAGAAGAAGAAG		583CAGTCACTGAGCTTATCCATGAGCCCTGGGTCACAATCTAG  258 ThrAlaProSer	547 GGGTCTTTÄÄIGTÄĞĞGTATATGGGĞÄÄTTTCÄÄ	544 GGA	GlyLeuLysAsn 	178 GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu       			LeuserLeuAspserIleTy              GATCTTAGCTTAGATAGTTTATT					30GluAlaThrSerAlaAlaThrValProThrThrPheTyrMet	1 ATGAAGTCTTTTTGTGATAATGATGATAATCATAGCAACACGACTAATTTGTTAGGG 21 PheSerLeuSerProHisMetLysMet	
n 325	Qy 643 8 305 Db 1606	S 285 Cy 624 I: B 285 Db 1546 A:	690 Qy 606 268 Db 1486	630 Qy 586 261 Db 1453	582 Qy 566 G1 al 257 Db 1452	546 Qy 546 1y 237 Db 1441	217 Qy 526 Va	197 QY 506 GI	177 Db 1402 504	157	141 Qy 446 I 141 Db 1291 AT 450	2y 426 Le 122 Db 1231 CT 399	103 Qy 406 103 Db 1171 351	93 Oy 386 83 Db 1111 291	63 Db 1051 GA	43 Db 991 G	60 Qy 326 T 29 Db 931 A	
1665	MetargProSerProAlaIleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp 662 :::::       :::::	eValAsnProIleGlyThrSerValThrSerTrpLeuProSerProThrValGln 642 	ProGluLysargGlyProSerLeuLeuPheProMetProProMetGluThrLys 623	ThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerSerArgGluAlaSer 605	yIleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerSerLysIleGly 585	IleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSerMetAlaLeuGlnAspLeuIle 565	The upneas maiser of serving in Grand and State of Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving Serving S			gllemetalaserserasmlementalagly-duhenalarightyshyshaspash 400	- ELYSPHEARGGINALBASHALAVAITHRASHUHEASHILESERATGINYASHVALGIL 465	UTYFLEUGLYThrPheSerTHGINGLUGIUA.AALAGIUA.ATYFAB9VALALAAIA 445	ArgHisHisGlpHisGlyArgTrpGlnAlaArgIIeGlyArgVarAlaGlyAsnLySasp 425				ThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaArg 345 :::	

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Qy 123LeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArg 141  Db 400 GATCTTAGCTTAGATAGTTTATTCTACAACACCACTCAFGAGCCCAACACG 450  Qy 142 AspLeuLeuSerGlnProPhe	Qy  64 AsnPheHisSerProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeu 83  11	21 61 30 121 44	Alignment Scores:  1.99e-132	US-10-059-911-38  Sequence 38, Application US/10059911  Publication No. US20030159180A1  GENERAL INFORMATION: APPLICANT: Fischer, Robert L. APPLICANT: Mizukami, Yukiko APPLICANT: The Regents of the University of California TITLE OF INVENTION: Methods for Altering Organ Mass in Plants FILE REFERENCE: 023070-090730US CURRENT APPLICATION NUMBER: US/10/059,911  CURRENT FILING DATE: 2002-06-17  NUMBER OF SEQ ID NOS: 42  SOFTMARE: PatentIN Ver. 2.1  SEO ID NO 38  LENGTH: 1668 TYPE: DNA ORGANIZM: Artificial Sequence PEATURE: OTHER INFORMATION: Description of Artificial Sequence:truncated or OTHER INFORMATION: mutated ANT CDNA transgene ANTMNLS  US-10-059-911-38
Oy  446	111 CATTTGAGAAGGAAGAAGCTGTTTCTCTAGGGGTGCTTCCATCTATAGAGGAGTCACA  406 ArgHisHisGlpHisGlyArgTrpGlnalaArgIleGlyArgValAlaGlyAsnLysAsp	326 931 346 366	AspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHis 28 :::	Qy 178 GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu 197

Percent Similarity: 54.52% Conservative: 78 Best Local Similarity: 43.50% Mismacches: 104 Best Local Similarity: 43.50% Indels: 218 Query Match: 14 US-10-024-632-2 (1-663) x US-10-059-911-4 (1-1738)  Cy 9 AsnThrAspAspGlyAsnAsnHisAsnTrpLeuGlyPheSerLeuSerProHisMet 27	(1)(1647) ORMATION: Canola AINTEGUMENTA (ANT) -4 res: 4.22e-131 Length: 1307.00 Matches:	TYPE: DNA TYPE: DNA ORGANISM: E FEATURE: OTHER INFOR OTHER INFOR FEATURE: NAME/KEY: C	VENTION: Methods for Altering Organ Mass in NCE: 023070-090730US LICATION NUMBER: US/10/059,911 ING DATE: 2002-06-17 EQ ID NOS: 42 atentIn Ver. 2.1	L-4 Application US/10059911 AND. US20030159180A1 CORMATION: Fischer, Robert L. Mizukami, Yukiko	Db 1606 CTTAAGACCGTCGCTCTTACTTTGCCTCAGATGCCGGTTTTCGCTGGGCTGAT 1662  Qy 663 Thr 663  1663 TCT 1665	624 IleValAsnProIleGlyThrSerValThrSerTrpLeuProS :::		eGly 585 145 aSer 605		526 1432	Db 1429 GAA 1431
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                                                      GTTTTCGCTGCGTGGGCTGATTCT 1644
                                                                              ValPheAlaSerTrpThrAspThr 663
                                                                                                           ACTACGAACCCTAATGCTGATCTCAAG---ACCGTTTCTCTTACTCTGCCGCAGATGCCG
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APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
FITIE OF INVENTION: Methods for Altering Organ Mass in Plai
FILE REFERENCE: 030070-090730US
CURRENT APPLICATION NUMBER: US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
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                                 GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu
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RESULT 12
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; Sequence 26, Application US/10059911
; Publication No. US20030159180A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; APPLICANT: The Regents of the Univer
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US-10-024-632-2 (1-663) x US-10-425-114-11685 (1-1231)
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
PILE REFERENCE: 38-21(53313)B GURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION UNMERS: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 11685
SEQ ID NOS: 73128
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
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ORGANISM: Glycine max
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421 ACCITIAGTACCCAAGAGGAAGCAGCTGAAGCCTAIGACATTGCTGCTATTAAATTCAGA
                                   430 ThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAlaIleLysPheArg 449
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                                                                                                                                                     HisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysAspLeuTyrLeuGly 429
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Kovalic, David K.
Screen, Steven E
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US-10-424-599-123485
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Pred. No.:
                                                                                                     ; OTHER INFORMATION: US-10-424-599-123485
                                                                                                                              APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated '
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 123465
LENGTH: 1949
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
FILE REFERENCE: STORE IN DAT METTRAG 225147 1
                                                                                                                                                                                                                                                                                                                                                                   Sequence 123485, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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-DB=EST -OFMT=fastap -SUFFIX=rst -MAYRIX-1010sm62 -TRANS-human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MAYRIX-1010 -THR_MIN=0 -ALICN=15 -MODE=LOCAL
-DCTALIGN=200 -THR_SCORE=p0t -THR_MAX=100 -THR_MIN=0 -ALICN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER-US10024632 @CGN 1 1 2135 @TUNAT 09032004 101208 10776 -NCPU=6 -ICPU=3
-USER-US10024632 @CGN 1 1 2135 @TUNAT 09032004 101208 10776 -NCPU=6 -ICPU=3
-NORMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LOWGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPDEXT=0.5 -FGAPOP=6
-DSPETT=7 -YGAPOP=10 -YGAPDEXT=0.5 -DELICP=6 -DELEXT=7
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-024-632-2
3502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              March 13, 2004, 00:45:08; Search time 2976 Seconds (without alignments) 6652.764 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Ygapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2004 Compugen Ltd.
                            em_estba:*
em_esthum:*
estin:*
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## 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

em estro

em_estfun:* em_estom:*

em_gss_hum:
em_gss_inv:
em_gss_pin:
em_gss_pin:
em_gss_fun:
em_gss_mam:
em_gss_mam:
em_gss_mam:
em_gss_mad:
em_gss_pod:
em_gss_pod:

em_estmu:*
em_estov:*
em_estpl:*

	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AW348127/c	RESULT 1
Bukaryota; Viridiplantae; Streptophyta; Emorpophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;	Glycine max	Glycine max (soybean)	BST.	AW348127.1 GI:6845837	AW348127	sequence.	GM210001A21A2 Gm-r1021 Glycine max cDNA cione Gm-r1021-4 3', mkNA	AW348127 752 bp mRNA linear EST 04-OCT-2000		

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451

391

638

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151

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598 331 518 571

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REFERENCE
AUTHORS
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scores:
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Other_ESTs: AI444013

Contact: Vodkin, L.O., PI, A Functional Genomics Program Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Illinois Prowin R. Madigan Building,
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                                                                                                IleSerArgTyrAspValGluArgIleMetAlaSerSerAspLeuLeuAlaGlyGluLeu 478
AlaArgArgLysLysAspAsnAspProArgAsnLysAspIleAspTyrAsnLysSerVal 498
                                                         ATTTCANNATACGNTGTNNNNNGAATCATNNNNAGTAGCAATCTCCTCGNNGGGGAGCTT
                                                                                                                                                                  GAAGCATACGATGTAGNNNCGATCAAATTTCGCGGNGCNNNNGCAGTCACAAACTTTGAC 691
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(217) 333-4582
l: l-vodkin@uiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="mar:1021"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
/note_"Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
/note_"Xite_"Year-1021 is a sequence-driven, reracked set
of the original library Gm-cl004 which was prepared from
root cDNA. The mRNA was isolated from entire roots of 8
day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Strateagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize
the cDNA. The Gm-cl004 library was constructed by Dr.
Paul Keim & Virginia H. Corvell, Department of Biology,
Box5640, Northern Arizona University, Flagstaff, AZ
86011, email: paul.keim@nau.edu, virginia.coryell@nau.edu
The contig analysis to select unique genes was performed
by the laboratory of Ernest Retzel, Computational Biology
Centers, University of Minnesota,

http://www.br.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.sch.mr.
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/cultivar="Williams"
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'lab_host="XL10-Gold"
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                                                                                                                                                                                                                                                                                                        Centro de Biologia Molecular e Engenharia Genetic
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharum officinarum
Eukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae, PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
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SCJFFL3C06D04.g Saccharum officinarum FL3 Saccharum officinarum GL0ne SCJFFL3C06D04 5', mRNA sequence.
                                                                                                                                        Email: parruda@unicamp.br
Clone distribution: clone distribution
through the Brazilian Clone Collection
http://www.bcccenter.fcav.unesp.br
Plate: C06 row: D column: 04
Seq primer: T7 Promoter Primer.
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              /organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
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/lab_nost="DHIOB"
/clone lib="Gaccharum officinarum FL3"
/clone lib="Gaccharum officinarum FL3"
/clone lib="Gaccharum officinarum FL3"
/clone lib="Gaccharum officinarum Inflorescence (Scm-long);
/note="Organ: Base of developing inflorescence (Scm-long)]. cDNA lass of developing inflorescence (Scm-long)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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Submitted (25-APR 2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TICR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of t. maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, lows teate, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                                                                                                                                              GGCGTCGGTTGCGTCGGCGCCCCCCCCCGCAGCCGGCTGCAGATCAGGATCACCAGCTT
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                               GCTGGGACGACGGTGGAGAACCCCGGCGCGCGGTGACC-
                                                                                                              GTGTGCGGCGAGCTGGGCAGCATCACAGCCAGGTTCTTGCGCCACTACCCGGCGGCGCCA
                                                                                                                                                      ---CysGlyGluLeuGlnSerLeuSerLeuSerMet--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
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/db_xref="MaizeDB:638053"
/db_xref="taxon:4577"
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Clone distribution: clone distribution
through the Brazilian Clone Collection
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Caixa Postal 6010, 13083-970, Camp
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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/note="Organ: Base of developing inflorescence (5cm-long);
/note="Organ: Base of developing inflorescence (5cm-long);
vector: pSport1; Site 1: Sal1; Site 2: NotI; An
unidirectional cDNA library generated from (Base of
developing inflorescence (5cm-long)); cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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Aspval:             31 GACGTTV   46:   TAT 54:   TAT 5	GluTyr' GAGTATO ArgGly' AGAGGTT AGAGGTT GGAAACL GGAAAACL	LYSGLUC	-2 (1-66 GlnProv        CAGCCTA	Scores: milarity: Similarity: h:

been generated by the Floral Genome Project (FGP). The Floral Genome Project is funded by NSF's Plant Genome Research Program (DBI-0115884). More information about the project can be obtained at http://fgp.bio.psu.edu"

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treptophyta; Embryo a; eudicotyledons; ; Fabaceae; Papilio	769 bp mRNA linear Hycine max cDNA clone SOYBBAN Llar to TR:Q9SYC2 Q9SYC2 F11M15		BPheArgGlyAlaAsnAlaValThrAsnPl 	euGlyThrPheSerThrGlnGluGluAl                       TTGGGACCTTTAGTACTCAGGAGGGAGC	ArghishisglnhisglyargTrpGlnAlaArgIl 	:gLysSerSerGlyPheSerArs 	.nValGlnLeuGluGluMetLys    :::           AGGAAGAACTTGAAGGGATGAAC	uAlaAlaLeuLysTyrTrpGl                 AGCAGCACTCAAATATTGGGGG	.rarglysG1yArgG1nVa1TyrLeuG1yG1yTyrAspMetG1uG1 	.YArgTyrGluAlaHisLeuTrpAsj 	SerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGl; 	Length: 545 Matches: 169 Conservative: 5 Mismatches: 7 Indels: 0 Gaps: 0
<pre>phyta; Tracheophyta; core eudicots; noideae; Phaseoleae; , Coryell,V.;</pre>	ear EST 04-DEC-2002 YBBAN CLONE ID: F11M15.6 PROTEIN. ;,		laValThrAsnPheAspIleSerArg 461 	luGluAlaAlaGluAlaTyr 441                 agggagcagcTgAAgcATAC 480	უ <u>—</u> წ	GIYAlaSerIleTyr 401           AGGCGCATCTATGTAT 360	AsnMetSerArgGln 381             JAACATGAGCAGACAA 300	ProSerThrHisIle 361	TyrAspMetGluGlu 341              TATGACATGGAAGAG 180	AspAsnSerCysLys 321                GACAATAGCTGTAAG 120	SerGlnTyrArgGly 301                TCTCAGTATAGAGGG 60	

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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This Clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www.resgen.com
Seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                            TTAAAATCATTGACATTATCCATGGGAAGTGGTAAGGATTCAACATGTGAAAACCAGTGGT
  {\tt LysLysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGlu}
                                                                      GlyValThrArgHisArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCys
                                                                                                                                              LysGlnProValHisArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArg 300
                                                                                                                                                                                                GAAAATAGCACAAACACTACTGTTGAAATA----- 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Gm-c1036"
//clone lib="Gm-c1036"
//note="Vector: pspoRT1; Site_1: Not1; Site_2: Sal1; This
//note="Vector: pspoRT1; Site_1: Not1; Site_2: Sal1; This
//note="Vector: pspoRT1; Site_1: Not1; Site_2: Sal1; This
cDNA library was constructed from mRNA isolated from
somatic embryos (age ranging from 2 months to 9 months)
cultured on MSD 20. The library convarient using the
cultured on MSD 20. The library convarient using the
cultured on MSD 20. The library construction
kit. Complementary DNA was synthesized from mRNA using a
poly (dT) sequence with a Not1 restrictions site. Sal1
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by Not1 digestion. The cDNA fragments
were directionally cloned into the Not1-Sal1 restriction
site of the pSPORT1 vector. The ligated cDNA fragments
were transformed into E.coli ElectroMax DH10B host cells.
This library was constructed in the laboratory of Dr. Lila
Vodkin by Anu Khanna at the University of Illinois at
Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="somatic embryos cultured
/lab_host="DH10B"
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/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1036-14361"
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398 CAAGAATTTGTTGCCGCCATTAGAAGAAAAGCAGTGTTTTCTCCAGGGGTGCATCAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 ACCAACTITCCAATTAGCAACTATGAGAAGGAATTGGATGAAACACATGACGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 ArgTyrAspValGluArgIleMetAlaSerSerAsnLeu---LeuAlaGlyGluLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 TyrAspValAjaAlaIleLysPheArgGlyAlaAsnAlaValThrAsnPheAspIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF510900 774 bp mRNA linear EST 09-SEP-200 CAbud0001 IIIR C03 Vitis vinifera cv. cabernet sauvignon (Clone 8) Bud - CABUD Vitis vinifera cDNA clone CAbud0001_IIIR_C03 3', mRNA
                                                                                                                                                                                                                                                                                                             CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
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CF510900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Jones,K. and Cook,D.
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                                                                                                                                                                                                  Seq primer: GCCAAACGAATGGTCTAG
Location/Qualifiers
                                                                                                                                                                                                                                               Email: drcook@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                             Contact: Douglas Cook, PhD
                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2003)
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                                                                                                                                                                                                                                                                  530 754 6561
530 754 6617
/db_xref="taxon:29760"

/clone="CAbud0001 IIIR_C03"

/sex="Hermaphrodite"

/dev_stage="Pre-bloom (10-11

/lab_host="DH5alpha"
                                                                                                             /organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:34542668
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-gnon (Clone 8)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 ArgGlnGlnGly-----HisMetSerValGlnThrHisProTyrTyrSerGlyLeuAla 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 ValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGluGlnGlnMetAsnCys 222
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TyrAspMetGluGluLysAlaAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGly
                                                                                                                                                   AspAsnSerCysLysLysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                      LysLeuGlyGlnLysGlnProValHisArgLysSerIleAspThrPheGlyGlnArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCATCGTTGATGACGGAGGAGCTCCTGGGTCTATTGGAGCTATGGGTTGTGGGGATTTA
                                                                                                            TCACAATATAGAGGAGTTACAAGGCATAGATGGACTGGTAGATATGAAGCCCATCTTTGG
                                                                                                                                                                                                                                                                                                           SerGlnTyrArgGlyValThrArgHisArgTrpThrGlyArgTyrGluAlaHisLeuTrp
                                                                                                                                                                                                                                                                                                                                                                            AAGGTTGCACAAAAGCAACCAGTTCATAGGAAGTCCATTGACACATTTGGGCAGAGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATTGCCATACCCAGATCCCTCCTATGGGGGAGGATGGAATGCCTTGCCTGAAAAACTGG
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SfiI; CABUT is a cNNA library of Vitis Vinifera cv.
'Cabernet Sauvignon' (Jone 8 dissected buds. Samples were
collected May 13, 2002 from pre-bloom plants (10-11 days
before bloom), pre-veraison. Sampled vines were located at
the University of Callifornia, Davis, Experimental
Vineyard. cDNAs were made by oligo-dT priming and
directionally cloned: 5'and 3' adaptors were used in
cloning as follows:
5'-ANGCAGTGGTATCAACGCAGAGTGGGCCATTACGGCCGGG-3' and
5'-ATCTACAGGCCGAGGGGGGCCACATG-dT(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Vitis vinifera cv. cabernet sauvignon (Clone
8) Bud - CABUD"
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79.23%
67.69%
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Best Local Similarity: Query Match:

Percent Similarity:

9.68e-73 855.00 70.63% 59.79% 24.41%

Mismatches: Indels: Conservative: Pred. No.:

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Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Generation of ESTs from abiotic stressed potato tissue Unpublished (2003)
Other ESTs: EST713100
Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CK267021 882 bp mRNA linear EST 12-DEC-2003 EST713099 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAC822 5' end, mRNA sequence.
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Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
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clone="POAC822"
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KEYWORDS
SOURCE
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DEFINITION
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                                                                                                                                               BJ188928 mRNA linear EST 17-0
BJ188928 normalized full length cDNA library, chloronemata,
caulonemata and malformed buds Physcomitrella patens subsp.
Physcomitrella patens subsp. Physcomitrella patens subsp.
                                                                          BJ188928.1
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                                                                                                                       cDNA clone pphb45d02 5', mRNA sequence.
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Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (http://www.brc.riken.go.jp/lab/spd/Eng/index.html). The database of Physcomitrella EST clones is available at the PHYSCObase (http://moss.nibb.ac.jp).
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Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Vichiyama, T., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tshini@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-FLC phage vector (Carninci et al.
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyh tail was
ligated to BanHI site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 81-559-81-6856
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                             AGAĀĀGGĀĀGGTCĀĀĀCTCGCĀĀĀGGTCGĀCĀĀGTĀTĀCTTĀGGĀGGĀTĀTGĀTĀĀĀGĀĀ
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/clone="pphb45d02"
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/sub_species="patens"
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BJT78045 normalized full length cDNA library, chloronemata, caulonemata and malformed buds Physcomitrella patens subsp. cDNA clone pphb21g12 5', mRNA sequence.
BJT78045
BJT78045.1 GI:18346002
EST.
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Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H.,
Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shino:
Kohara,Y. and Hasebe,M.
Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for la
                                                                                                                                                                                                                                                                                                                                                                                                                                         Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Enyscomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryoph
Eukaryota; Viridiplantae; Funariales; Funariaceae;
Bryopsida; Funarialae; Funariales; Funariaceae;
                                                                                                                                                                                                                                 Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                               evolution
Protonemata were blended by the POLYTRON, ar
the BCDATG medium for 13- 14 days under the
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RESULT 10 BJ178045 LOCUS

DEFINITION

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VERSION KEYWORDS

ACCESSION

REFERENCE

AUTHORS

TITLE

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genes

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Percent Similarity:
Best Local Similarity:
Query Match:
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748 bp mRNA linear EST 2 psHB023xF07f USDA-IFAFS:Expression of Phytophthora sojae during infection and propagation Phytophthora sojae cDNA sHB023F07 5, mRNA sequence.
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/mol_type="mRNA"
/mol_type="mRNA"
/sub_species="patens"
/db xref="taxon:145481"
/clone="pphb21g12"
/tissue_type="mixture of chloronemata, caumalformed buds"
/clone_lib="normalized full length cDNA lichloronemata, caulonemata and malformed bu
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1 (bases 1 to
Tyler, B.
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CF807326.1
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BACKWARD: BK reverse primer
Plate: 023 row: F column: 07
Seq primer: BK reverse primer
High quality sequence stop: 748
Location/Qualifiers
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Contact: Tyler
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Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
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Tel: 540-231-7318
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                                                      GlnGluTyrValAlaHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIle
                                                                                               ACCAACTTTCCCATCTATGAGAAGGAACTGGAGAGATGAAGAACATGACCAGG
                                                                                                                            IleAsnPheSerIleGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArg 380
                                                                                                                                                          GATAAGGCAGCCAGGGCTTACGATCTCGCAGCTCTCAAGTACTGGGGTCCAACTACCACC
                                                                                                                                                                               GluLysAlaAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHis 360
                                                                                                                                                                                                                           AGAAGAGAAGGCCAAAGCAGGAAAGGAAGACAAGTTTACCTGGGTGGTTATGACAAGGAA
                                                                                                                                                                                                                                                                                          GGCGTCACCCGACATAGATGGACGGGAAGATACGAAGCTCATCTATGGGACAATAGTTGT
{\tt TyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgVal}
                                   CAAGAGTTTGTTGCTTCTACGAAGGAAGAGCAGTGGTTTCTCTAGGGGGGGCCTCTATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone lib="USDA-IFAFS:Expression of Phytophthora sojae
genes during infection and propagation"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="mycelium"
/cell_line="P6497"
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

spermatophyta; Magnoliophyta; eddicotyledons; core eddicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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sah25f05.y1 Gm-c1036
ID: Gm-c1036-2554 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available through: ResGen, In South Memorial Parkway Huntsville, AL 35801 call: (800)-533-4363 or contact via email: High quality sequence stop: 431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYTASPValAlaAlaIleLysPheArgGlyAlaAsnAlaValThrAsnPheAspIleSer
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/clome_lib="Gm.cl036"
/clome_lib="Gm.cl036"
/clome_lib="Gm.cl036"
/note="Vector: psPoRTI; Site 1: NotI; Site 2: SalI; This
/note="Vector: psPoRTI; Site 1: NotI; Site 2: SalI; This
cDNA library was constructed from mRNA isolated from
somatic embryos (age ranging from 2 months to 9 months)
cultured on MSD 20. The library was prepared using the
life Technologies psuperscript cDNA library construction
kit. Complementary DNA was synthesized from mRNA using a
poly (dT) sequence with a NotI restrictions site. SalI
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-SalI restriction
site of the psPoRTI vector. The ligated CDNA fragments
were transformed into E.coli ElectroMax DH10B host cells.
This library was constructed in the laboratory of Dr. Lila
Vodkin by Anu Khanna at the University of Illinois at
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"

/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1036-2554"
/tissue_type="somatic embryos cultured on MSD 20"
/lab_host="DE108"
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e, AL 35801 For further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccu@resgen.com
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Glycine max (soybean)

Glycine max

Glycine max

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Phaseoleae;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                AW200688 644 bp mRNA linear EST 02-DEC-2001 se92c07.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-229 5' similar to TR:Q41832 Q41832 OPEN READING FRAME. ;;
1 (bases 1 to 644)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
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Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 968 Std Error: 0.00
High quality sequence stop: 418.
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Contact: Shoemaker R/Public Soybean EST
Public Soybean EST Project
Washington University School of Medicine
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/mol type="mRNA"

/db_xref="teaxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-229"

/tissue_type="cotyledons of 3- and 7-day-old Williams
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/lab_host="DH10B"
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y 281 LysGlnÞroValHisArgLysSerIleAspThrÞheGlyGlnArgThrS	S-10-024-632-2 (1-663) x AW200688 (1-644)	B: 10 Gaps: 0	uery Match: 23.04% Indels: 0	:y: 84.09% Misn	92.61% Conservative:	807.00 Matches: 1	2.82e-68 Length: 6	Scores:
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114 CAGAAACCCTCTCCAAAGAAAACCGTCGACACCTTCGGCCAACGACCACCTCCATCTACCGC erGlnTyrArg 300 173

tissue_type="cotyledons of 3- and 7-day-old Williams"

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REFERENCE
AUTHORS
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Tel: 314 286 1800
Fax: 314 286 1810
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8175e07.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1027-7165 5' similar to TR:Q41832 Q41832 OPEN READING FRAME. ;,
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EST.
Glycine max (soybean)
                                                                                                                                    Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 412.
                                                                                                                                                                                                                                                                                                       Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysLysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGlu 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyValThrArgHisArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCys 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATGACATTGCTGCTATCAAATTCAGGCGATTAAATGCAGTCACAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaGlyAsnLysAspLeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAla 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgVal 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAAGAGÁAGGCCAÁAGCÁGGAÁAGGÁCAAGTTTACCTGGGTGGTTATGÁCAAGGÁA 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACAGAGGAGTGACGAGACACCACCAGCATGGCCGATGGCAGGCGAGAATAGGCAGAGTT 533
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                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 Louis, MO 63108, USA
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δ	294 GlnArgThrs	erGlnTyrArgGly	GlnArgThrSerGlnTyrArgGlyValThrArgHisArg	TrpThrGlyArgTyrGluAla	313
οd	3 GAGCGCACCT	CCATCTACCGCGGC	GTCACCCGACATAGA	GAGCGCACCTCCATCTACCGCGGCGTCACCCCGACATAGATGGACGGGAAGATACGAAGCT	8
Q	314 HisLeuTrpA	spAsnSerCysLys]	LysGluGlyGlnThr.	HisLeuTrpAspAsnSerCysLysLysGluGlyGlnThrArgLysGlyArgGlnValTyr	333
Db	63 CATCTATGGC	ACAATAGTTGTAGAJ	AGAGAAGGCCAAAGC	CATCTATGGGACAATAGTTGTAGAAGAGAAGGCCAAAGCAAAGGAAAGGAAGG	122
Qy	334 LeuGlyGly7	YrAspMetGluGluI	LYBAlaAlaArgAla	LeuGlyGlyTyrAspMetGluGluLysAlaAlaArgAlaTyrAspLeuAlaAlaLeuLys	353
Дb	123 CTGGGTGGTT	ATGACAAGGAAGATI	AAGGCAGCCAGGGCT	CTGGGTGGTTATGACAAGGAAGATAAGGCAGCCAGGGCTTACGATCTCGCAGCTCTCAAG	182
Q	354 TYrTrpGly	roSerThrHisIle	AsnPheSerIleGlu  }	TyrTrpGlyProSerThrHisIleAsnPheSerIleGluAsnTyrGlnValGlnLeuGlu	373
В	183 TACTGGGGT	CAACTACCACCACC	PACTITCCCATTICC	TACTGGGGTCCAACTACCACCAACTTTCCCATTTCCAACTATGAGAAGGAACTGGAG	242
82	374 GluMetLys/	\snMetSerArgGln	GluTyrValAlaHis	GluMetLysAsnMetSerArgGlnGluTyrValAlaHisLeuArgArgLysSerSerGly	393
Db	243 GAGATGAAGA	ACATGACCAGGCAA	GAGTTTGTTGCTTCT	GAGATGAAGAACATGACCAGGCAAGAGTTTGTTGCTTCTCTACGAAGGAAG	302
Qy	394 PheserArg	31yAlaSerIleTyr	ArgGlyValThrArg	PheSerArgGlyAlaSerIleTyrArgGlyValThrArgHisHisGlnHisGlyArgTrp	413
Вþ	303 TTCTCTAGG	GGGCCTCTATATAC	AGAGGAGTGACGAGA	TTCTCTAGGGGGGCCTCTATATACAGAGGAGTGACGAGACACCAGCATGGCCGATGG	362
ę Y	414 GlnAlaArg	leGlyArgValAla	GlyAsnLysAspLeu	GlnAlaArgIleGlyArgValAlaGlyAsnLysAspLeuTyrLeuGlyThrPheSerThr	433

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REFERENCE
AUTHORS
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Shoemaker,R., Keim,P., Warra,M., Hillier,L., Kucaba,T., Martin,J.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Beck,C., Wylie,T., Waller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU964897

Sat04a07.yl Gm-c1036 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1036-12685 5' similar to TR:Q9SYC2 Q9SYC2 F11M15.6 PROTEIN.;,
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Fax: 314 286 1810
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Seq primër: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 445.
Location/Qualifiers
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//clone lib="Gm-Cl036"
//clone lib="Gm-Cl036"
//clone lib="Gm-Cl036"
//clone library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the cultured on MSD 20. The library was prepared using the cultured on MSD 20. The library was prepared using the cultured construction wit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restrictions site. Sall linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-Sall restriction site of the psPOPRT vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. This library was constructed in the laboratory of DT. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. e-mail: 1-vodkin@uiuc.edu"
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			AGCC	uArg	GATA	_a_i_e	TCTT	  - -	AAGG	rArg	igco	aHis	TAGT	eGlu	GICIT	gA1a	ATCAA	nThr	TAGA	8Arg	BU964897	72# 72# 70-67	
			ATCC	IleMe	AAGT	Lysp	TACT		CATC	Hish	ATTA	LeuA	AACT	AsnT	TATG	TYEA	AGAA	ArgL	TGGA	Tzgī			
			TTGA	lGluArgIleMetAlaS	TCAG	TyrAspValAlaAlaIleLysPheArgGlyAlaAsnAlaValThr.	caggaaachaagarctitráctitéggaactiticagtactgaagaagaggctgctgaag	euG1	ACCA	18G1:	GAAG	rgAr	ATGA	γrGln	ATTT	spLe:	AGAAGGGAAGGCAATCAAGAAAAGGACGCCAAGTTTAT	ysG1:	CTGG	lyValThrArgHisArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSe	(1-552	013035	
			AAGC.	— <b>ი</b>	AGGT	gGly.	AACT	YTHE	ACAC	nHis	GAAA	  skyg	GAAG	nValo	PGCI(	AlaAla	1000	Argo	AGG	Arg		Length: Matches: Conservat Mismatche Indels: Gaps:	
			AACA	rSerAsnLeu-	CTCA	AlaAı 	TTCA	Phes	3GAA	31 ya.	AGCA	Gers.	BAAT	GlnLeuGluGlu	3CAC:	laLe	AAGT	31nVe	ATG	YzG]		: vati ches	
			CTCT	anLe:	cec	SnAl	TAC		ATG	17. 17. 18.	iree	erGly	rGGA	uGlu	GAAC	av.Tu	TTAT	TYT.	AGCT	LAT La		: ve:	
			CCA	-	GIO	1Va1	GAAG	rGlnG	GCAAC		CITICI	Phes	GAA	G1u	TACT	- TYT	TIGG	Leuc	CACC	Hisi		146 20 15 15	
			ATAG	LeuAl	CAA	Thra.	3AAG	=1 uG	GCAAC	llaAı	CCA	GerA	TGAJ	letT)		-01 -12 -13	GTGC	11YG1	TTTC	-ull			
			3AGG/	LaGly	CTT	AsnPheAspIleS	GGCT	L LAL	AATT	9116	666	-gG1	ACAC	/sAsnMe	GAC	yPro	ATAT	Y	GGAT	J I I I		,	
			AGGA	-Glui	IGAC/	Aspi	GCT	lAla(	rgect	G1 y2	rica	Alas	ATG		TCCF	SerT	GATA	Asp	AATA	Asns			
			CGTGAAAGCCATCCTTGAAAGCAACACTCTCCCAATAGGAGGAGGAGGAGCTGCA	aGlyGluLeuAl	GACATAGCTGCGATAAAGTTCAGAGGTCTCAACGCTGTCACAAACTTTGACATGAG	)IleSe	SÁAGC	aGlyAsnLysAspLeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAl	TATCGTGGAGTTACAAGGCATCACCAACACGGAAGATTGGCAAGCAA	TyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgVa	CAAGAATTTGTTGCTGCCATTAGAAGGAAAAGCAGTGGTTTCTCCAGGGGTGCATCAATG	GlnGluTyrValAlaHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIle	ACCAACTTTCCAATTAGTAACTATGAGAAGGAATTGGATGAAATGAAACACATGACGCGA	SerIleGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArg	CAGCTAGGTCTTATGATTTAGCTGCACTGAAGTACTGGGGGGACATCCACCACT	aAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHi	TTGGGTGGATATGATAAAGAA	LysLysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGlu	TAACGCGACATAGATGGACTGGAAGGTATGAAGCTCACCTTTGGGATAATAGCTG	=ÿ		•	
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Search completed: March 13, 2004, 07:59:35 Job time : 2990 secs

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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/ cgn2_6/ptodata/1/pubpaa/US08_PUB.COMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUB.COMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Sequence 5, Appl
Sequence 13, Appl
Sequence 11, Appl
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nc	equence 42, App	equence 8, App	equence 24, App	equence 12, App	equence 1310, A	equence 1312, A	equence 13, App	equence 1743; A	equence 1313	equence 1314, A	equence 16, App	equence 2164, A	equence 140, Ap	equence 1311, A	equence 3, Appl	equence 202, Ap	equence 34, App	equence 6, Appl	equence 104, Ap	equence 154, A	equence 1765, A	equence 14, App	equence 19, App	equence 23, App	equence 346, Ap	equence 2496, A	equence 400, Ap	equence 25, Ar	equence 17, App

## ALIGNMENTS

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SEQUENCE 2, Application US/10024632
Publication No. US20020170093A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
APPLICANT: Nonsanto Technology LLC
APPLICANT: Nonsanto Technology LLC
APPLICANT: Dotson, Stanton B.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION
TITLE OF INVENTION AND ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION
TITLE O
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Best Local Similarity
                                                                                         121 RGLSLDSIYYNSQNAEAQPNRDLLSQPPRQQGHMSVQTHPYYSGLACHGLYQAPLEEETT 180
121 RGLSLDSIYYNSQNÁEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETT 180
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Result No.

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APPLICANT: MONSANCO TECHNOLOGY LLC
APPLICANT: He, Steve S.
APPLICANT: Dotson, Stanton B.
APPLICANT: Dotson, Stanton B.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL
TITLE OF INVENTION: GROWTH AND USES THEREOF
FILE REFERENCE: 38-21(51837)B
CURRENT APPLICATION NUMBER: US/10/024,632
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR FILING DATE: 2000-12-21
NUMBER OF ESG ID NOS: 33
SOPTWARE: Patentin version 3.1
SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: Glycine m
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US-10-024-632-4
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Publication No. US20020170093A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 379; Conserv
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                                                                                                        MKSMENDDNADLNNQNNWLGFSLSPQMHNIGVSSHSQPSSAAEVVPTSFYHHTAP--LSS 58
                                                       FGMCYGV-GENGNFHSPLTVMPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDFLGGATM 111
             ygfyygleaenvglysalpimplksdgslygletisksqaqamattstpklenflggeam
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                                                                                                                                                                                                         49.0%; Score 1715; DB 13; 54.4%; Pred. No. 2.2e~151; tive 84; Mismatches 166;
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; Sequence 6, Application US/10024632
; Publication No. US20020170093A1
; GENERAL INFORMATION:
APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
APPLICANT: Dotson, Stanton B.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITT
TITLE OF INVENTION: GROWTH AND USES THEREOF
FILE REFERENCE: 38-21(51837)B
; CURRENT APPLICATION NUMBER: US/10/024,632
; CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR APPLICATION NUMBER: US 60/257,896
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Matches 341
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                                                                                      GNNHNWLGFSLSPHMKMEATSAATVPTT------
  YMSPSQSHL-
                                               GGSSNWLGFSLSPHMPAMEVPSSSEPSTAAHHHHHHHPPAAAAAAGAMSSPPDSATTCNF
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                                                                                                                                                  40.2%; Score 1408.5; DB 13; Length 642; 46.5%; Pred. No. 1.1e-122; tive 64; Mismatches 149; Indels 179;
  -SNFGMCYGVGEN--GNFHSPLTVMPLKSDGSLCILEALKRSQTQ 92
                                                                                                                                                                                                 Length 642
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                                                ; ORGANISM: Oryza
US-10-024-632-9
                                                                                                            APPLICANT: Dotson, Stanton B.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: GROWTH AND USES THEREOF
FILE REFERENCE: 38-21(51837)B
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US/10/024,632
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                Sequence 9, Application US/10024632
Publication No. US20020170093A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology LLC
APPLICANT: He, Steve S.
Query Match
Best Local Similarity
                                                                                  TYPE: PRT
                                                                                                   ENGTH: 669
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Score 1349.5; DB 13; Pred. No. 4e-117;
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Publication No. US20030159180A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
APPLICANT: Westhods for Altering Organ Mass in Plants
                                                      FILE REFERENCE: 023070-090730US
CURRENT APPLICATION NUMBER: US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                       LENGTH: 555
TYPE: PRT
         ORGANISM: Arabidopsis thaliana
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Best Local
Sequence 21, Application US/10059911
Publication No. US20030159180A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California APPLICANT: OF INVENTION: Methods for Altering Organ Mass in FILE REFERENCE: 023070-090730US
CURRENT APPLICATION NUMBER: US/10/059,911
CURRENT FILING DATE: 2002-06-17
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Pred. No. 3.1e-115;
9; Mismatches 113;
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      US-10-059-911-22
; Sequence 22, Application US/10059911
; Publication No. US20030159180A1
; GENERAL INFORMATION:
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US-10-059-911-21
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 21
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Best Local Similarity
Matches 312; Conserv
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                     STPERLLSFPAIFALPQVNQXWFGSNWGGNMSPWTSNPNAELK-TVALTLPQMPVFAAWA
                                                                                                        SPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT
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Pred. No. 2.2e-114;
0; Mismatches 114;
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APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
ITITE OF INVENTION: Methods for Altering Organ Mass in Plar
ITITE OF INVENTION INCHES FOR ALTERING ORGANIS
CURRENT APPLICATION NUMBER: US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 555
TYPE: PRT
ORGANISM: Artificial Sequence
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PEATURE:

OTHER INFORMATION: Description of Artificial Sequence:structurally
OTHER INFORMATION: altered ANT protein ANTMRII, temperature sensiti
OTHER INFORMATION: mutant
US-10-059-911-22
                                                                                                                                                      545 KIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREA 604
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                               STPERLLSFPAIFALPQVNQKMFGSNMGGNMSPWTSNPNAELK-TVALTLPQMFVFAAWA
                                                                        SPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT 661
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Pred. No. 7.9e-114;
70; Mismatches 115;
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(Sequence 5, Application No. US20030159180A1)
(GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass in Plar
FILE REFERENCE: 023070-090730US
CURRENT APPLICATION NUMBER: US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 548
TYPE: PRT
ORGANISM: Brassica napus
FEATURE:
OTHER INFORMATION: Canola AINTEGUMENTA (ANT)
US-10-059-911-5
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                                                                                                                                                                                                                                                   RQEYVAHLRRKTSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAE
                                                                                                                                                                                                                                                                                       ROEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAE
                                                                                                                                                                                                                                                                                                                               FKKEGHSRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFSVENYQKEIDDMKNMT
                                                                                                                                                                                                                                                                                                                                                                          CKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNWS
                                                                                                                                                                                                                                                                                                                                                                                                                     TTTMAAAAAKKKRGQEVVVGQKQIVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GGSTNVGVYGEFQQSLSLSMSFGSQSSCTTASHHHQNQTQNHQQISEALVETSAGFE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGN 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -FGTHHHNTSHKEAMDLSLDSLFYNTTHA---PNNNTNFQEF----FSFPQTRNHH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMGTHEYG-SHERG--LSLDSIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVG-ENGNTHSPLTVMPLKSDGSLCILEALKRS-----QTQVMVPTSSPKLEDFLGGA
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                                                                              RNISDEEAALTAVVNGGSNKEV---
                                                                                                                       TSVNNEE---TVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSDQKIMNCGNYRNSA
                                                                                                                                                                  AYDVAAIKFRGTNAVTNEDITRYDVDRIMASNTLLSGEMARRNS--
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MPPMETKI -- VNPIGISVISWLPSPIVQMRPSPAISLSHLPVFASWIDI 663

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APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: Mizukami, Yukiko
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
ITILE OF INVENTION: Methods for Altering Organ Mass in Plan
FILE REFERENCE: 023070-090730US
CURRENT APPLICATION NUMBER: US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 452
TYPOED: DDM
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US-10-059-911-13
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Matches 275;
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                                                                                                                                                                                                                                                                                                                                                   QQMNCGMGNERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTAPS-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFFG----THHNNTSHKEAMDLSLDSLFYNTTH---EPNTTTNFQEFFSFPQTRNH----
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                                                                                                              IENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNK
                                                                                                                                                                                             HRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMBEKAARAYDLAALKYWGPSTHINFS
DLYLGTFGTQEEAAEAYDVAAIKFRGTNAVTNFDITRYDVDRI
                             DLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERI
                                                                             AENYQKE1EDMKNMTRQEYVAHLRRKSSGFSRGAS1YRGVTRHHQHGRWQAR1GRVAGNK
                                                                                                                                                                                                                                                                                                                  -----GSFNVGV-----YGEFQQSLSLSMSPGSQSSCITGSHHHQQNQNQNHQSQNH 229
                                                                                                                                                          HRWTGRYEAHLWDNSFKKEGHSRKGROVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.2%; Score 1233.5; DB 14; 52.6%; Pred. No. 1.6e-106; ative 42; Mismatches 79; I
                                                                                                                                                                                                                                                                        -GTDSVAVDAKKRGH---AKLGQKQPVHRKSIDTFGQRTSQYRGVTR 304
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RESULT 10 US-10-059-911-9 ; Sequence 9, Application US/10059911 ; Publication No. US20030159180A1

> RESULT 11 US-10-024-632-11

Sequence 11, Application US/10024632 Publication No. US20020170093A1 GENERAL INFORMATION:

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LENGTH: 473
TYPE: PRT
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APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass in I
FILE REFERENCE: 023070-090730US
CURRENT APPLICATION UNMERS: US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
CORTENANCE DEFORMATION.
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Best Local Similarity
Matches 286; Conserva
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                                                                                                                                                                                                                                  GANAVTNFDISRYDVERIMASSNLLAGELARRKKDNDPRNKDIDYNKSVVTSVNNEETVQ 509
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NMGGNMSPWTSNPNAELK-TVALTLPQMPVFAAWADS
                               PIGISVISMLPSPIVQMRPSPAISLSHLPVFASWIDI
                                                                                                                                                                  VQAGNININENDSEWKMVLFNHPSQQQQANGINGSDQKIMNCGNYRNSAFSMALQDLIGIDS
                                                                                                                                                                                                       GTNAVTNEDITRYDVDRIMSSNTLLSGELARRN------NNSIV--VRNTE---
                                                                                                                                                                                                                                                                       KSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAEAYDVAAIKFR
                                                                                                                                                                                                                                                                                                                                                                                                              RGQEDVVVVGQKQIVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSFKKEGHSRKG
                                                                                                  VGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSL--LFPMPPMETKIV-N 626
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44.9%; Pred. No. 1.3e-105;
tive 56; Mismatches 89;
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APPLICANT: He, Steve S.
APPLICANT: Detacon, Stanton B.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION
TITLE OF INVENTION: SCHOOL MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION
TITLE REPERENCE: 38-21(51837)B
CURRENT APPLICATION NUMBER: US/10/024,632
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ 1D NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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ORGANISM: Gossypium hirsutum
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                                                                                                                568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452 NAVTNEDISRYDVERIMASSNILAGELARRKKDNDFRNKDIDYNKSVVTSVNNEETVQVQ 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 LEQQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGSQSSCVTAPSGTDSVA----VDAK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 VQTHPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
                                                                                                             LGN---
                                                                                                                                                                                                                       DKFGIG-----GDYSHHG-YFSLKGSKYEDGNSETDNSNENR---
                                                                                                                                                                                                                                                                        DSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIVNP 627
                                                                                                                                                                                                                                                                                                                            SGEASDELADMYWTA---NSDEQQQHQSTNTNNDASLANSSS-RNSSNPQSPKGSIGLAS 531
                                                                                                                                                                                                                                                                                                                                                                            AGNININE-NDSEWKMVLFNHPSQQQ-QANGNGSDQKIMNCGNYRNSAFSMALQDLIGI-- 567
                                                                                                                                                                                                                                                                                                                                                                                                                                SAVTNEDISRYDVKRICSSSTLIGGELAKRSPKDTASIAPEDYN-SCASSASPQPLLAIP 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGFSRGASVYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFRGT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGFSRGASIYRGVTRHHOHGRWOARIGRVAGNKDLYLGTFSTOEBAAEAYDVAAIKFRGA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYLGGYDKEEKAAKAYDLAALKYWGPTTHINF PLSTYEKELEEMKNMTRQEFVAHLRRKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRPVGKNLTRESVPRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRGHAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQ 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ASGNETNNNF----NFQALSLTMSP----TSRNGFPAIAPLEVVDNR 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQCDPNPNHNQRSGVHHVPFESATS------VSGFKSWLRQT-PFPGGK-- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HENQNTVPSPTRINVNVAPNYSSSGDAEAAENFTNPSSFIQTYRNYNENPQTLMAGGHSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HER-----RDLLSQP--FRQQGHMS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGSLCILEALKRSQT------QVMVPTSSPKLEDFLG----GATWGTHEY-GS 118
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41.7%; Pred. No. 2.2e-101;
tive 79; Mismatches 164; Indels 163;
                                                                                                                -LGLVHKIPMFALWNE 585
Sequence 10, Application US/10059911

Publication No. US2030159180A1

GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass in Plar
FILE REFERENCE: 023070-090730US
CURRENT APPLICATION UNMBERS US/10/059,911

CURRENT FILING DATE: 2002-06-17

NUMBER OF SEQ ID NOS: 42
SOFTMARE: Patentin Ver. 2.1

SOFTMARE: Patentin Ver. 2.1
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US-10-059-911-15

Plants

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Sequence 15, Application US/10059911

Publication No. US20030159180A1

GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass in Plar
FILE REFERENCE: 023070-090730US
CURRENT APPLICATION NUMBER: US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 370
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER THEORYPATTON: Description of Artificial General Sections
FEATURE: Theorypathon.
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RESULT 13
US-10-059-911-10
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US-10-059-911-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.3%; Score 1129.5; DB Best Local Similarity 56.4%; Pred. No. 6.5e-97 Matches 247; Conservative 29; Mismatches 5
                                                                                               353
                                                                                                                                          450
                                                                                                                                                                                                                                       390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 THVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGEL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSVMPLRSDGSLCLMEALNRSSHSNHHQDSSPKVEDFFG----THHNNTSHKEAMDLSLD
                                                                                                                                                                                                                     KSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFR
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                                                                                               GINAVINFDITRYDVDRI 370
                                                                                                                                       GANAVINEDISRYDVERI 467
                                                                                                                                                                                                                                                                                  ROVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFSAENYOKEIEDMKNMTRQEYVAHLRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSLSLSMSPGSQSSCITGSHHHQQNQNQNHQSQNHQQISEALVETSVGFETTTMAAAKKK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLFYNTTH---EPNTTTNFQEFFSFPQTRNH-----REET--R
                                                                                                                                                                                       KSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAEAYDVAAIKFR
                                                                                                                                                                                                                                                                                                                                                                            RGQEDVVVVGQKQIVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSFKKEGHSRKG
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:structurally
; OTHER INFORMATION: altered ANT protein ANTDN2
US-10-059-911-10
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US-10-059-911-11
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OTHER INFORMATION:
US-10-059-911-11
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Best Local Similarity 54.0
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10059911 publication No. US20030159180A1 GENERAL INFORMATION:
                                                                                                                              Query Match
Best Local &
                                                                                                                Matches 198;
                                                                                                                                                                                                                                                                                                                                APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass in |
FILE REFERENCE: 023070-090730US
FULL REPERENCE: 023070-090730US
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTMARE: Patentin Ver. 2.1
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                          IQ ID NO 11
IN THE TOTAL TO TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 EGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 VAVDAKKRGH---AKLGOKOPVHRKSIDTFGORTSOYRGVTRHRWTGRYEAHLWDNSCKK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 YVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYD 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503 NNEETVQVQAGNNNNENDSEWKMVLFNHFSQQQQANGNGSDQKIMNCGNYRNSAFSMALQ 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VAAIKFRGTNAVTNFDITRYDVDRIMSSNTLLSGELARRN------NNSIV--V
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                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOKMFGSNMGGNMSPWTSNPNAELK-TVALTLPOMPVFAAWADS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLYTSLSSSREASPEKRGPSL--LFPMPPM 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAAIKFRGANAVINFDISRYDVERIMASSNILAGELARRKKUNDFRNKDIDYNKSVVISV 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAEAYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWTDT 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGHSRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFSAENYQKEIEDMKNMTRQE
WGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQ 414
                                                                       RTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMSEKAARAYDLAALKY
                                         RTSQYRGVTRHRWTGRYEAHLWDNSFKKEGHSRKGRQVYLGGYDMEEKAARAYDLAALKY
                                                                                                                Conservative
                                                                                                                                                                                                       Description of Artificial Sequence:structurally altered ANT protein ANTDN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.8%; Score 1042; DB 14; 54.0%; Pred. No. 7.7e-89; tive 36; Mismatches 48;
                                                                                                                                27.3%;
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                                                                                                                34;
                                                                                                                Score 955.5; DB 1
Pred. No. 8.3e-81;
4; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -VVEGGSNKEVSTPERLLSFPAIFALPQV 265
                                                                                                                                                      DB 14;
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RESULT 15 US-10-374-780A-334 Sequence 334, Application US/10374780A Publication No. US20040019927A1 SOFTWARE: PatentIn SEQ ID NO 334 PRIOR APPLICATION NUMBER: 10/:
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906 PRIOR PRIOR PRIOR PRIOR PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847 CURRENT APPLICATION NUMBER: US/10/374,780A CURRENT FILING DATE: 2003-02-25 TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES FILE REFERENCE: MBI-0047 CIP APPLICANT: APPLICANT: APPLICANT: Sherman, Bradley K APPLICANT: APPLICANT APPLICANT: PRIOR PPLICANT: APPLICANT: TYPE: PRT ORGANISM: Arabidopsis thaliana FEATURE: LENGTH: 574 APPLICATION NUMBER: 10/171,468 FILING DATE: 2002-06-14 APPLICATION NUMBER: 09/934,455 FILING DATE: 2001-08-22 APPLICATION NUMBER: 60/336,049 FILING APPLICATION NUMBER: 1 APPLICATION NUMBER: 10/225,066 FILING DATE: FILING DATE: 2001-08-09 APPLICATION NUMBER: 60/338,692 INFORMATION: Riechmann, Jose J Jiang, Cai-Zhong Pilgrim, Marsha L Dubell III, Arnold T Keddie, James Broun, Pierre E Haake, Ratcliffe, Oliver Creelman, Robert A Heard, dam, Luc J DATE: 2002-08-09 ineda, Omaira Guo-Liang Volker Jacqueline E 2001-11-19 Lymne Jose Luis 10/225,068 10/225,067 IN PLANTS

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Search completed: March 9, 2004, 10:52:46 Job time : 40 secs
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                                                                                                                       533 E-----FPTVKTDYDMPSSDGTGGYSGWTSESVQ-GSNPG-----GVFTMWNE 574
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